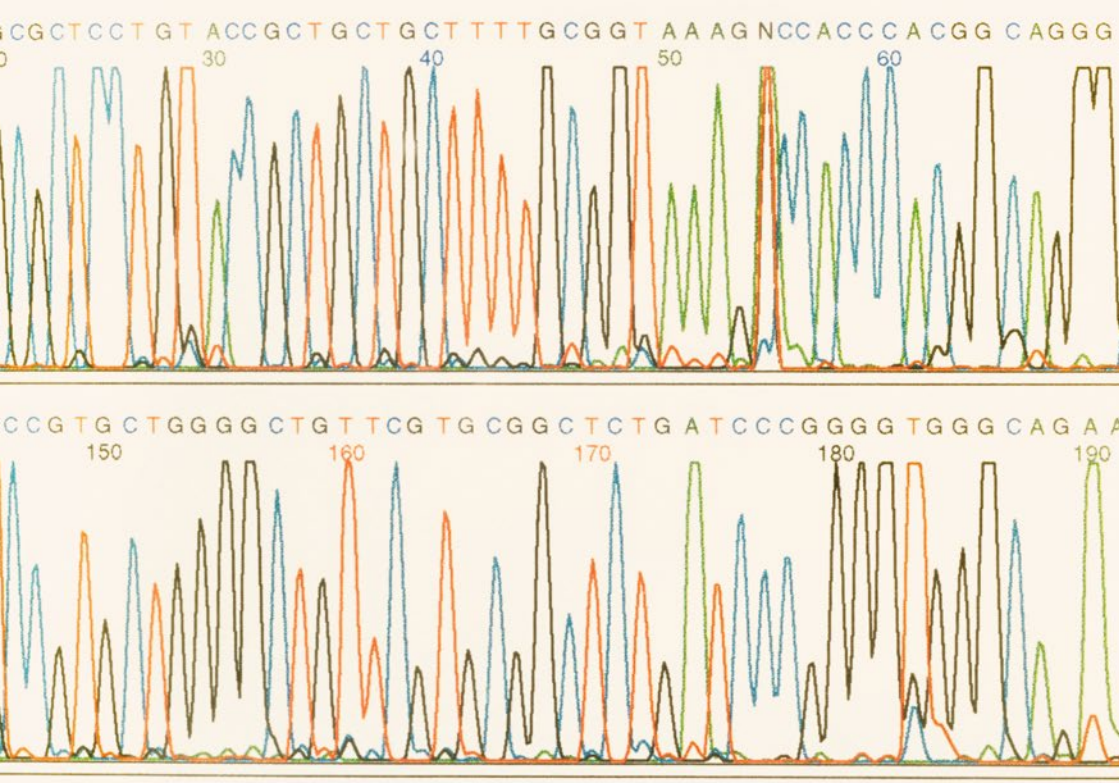

Population Genetics and Belonging

A Cultural Analysis of Genetic Ancestry

VENLA OIKKONEN

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* * *

Some of the chapters draw on my previously published work. Chapter 2 builds on "Mitochondrial Eve and the Affective Politics of Human Ancestry," published in *Signs: Journal of Women in Culture and Society* 40.3 (2015): 747–772. Parts of Chaps. 3 and 4 develop analysis initially published in "Kennewick Man and the Evolutionary Origins of the Nation" in *Journal of American Studies* 48.1 (2014): 275–290. I thank the University of Chicago Press and Cambridge University Press for permission to include the work here.

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1

Studying Population Genetics and Belonging

In the past 20 years, a number of biotechnological practices have emerged around the field known as "human population genetics." Transnationally framed scientific initiatives such as the Genographic Project or the HapMap Project have sought to identify genetic variation across world populations. Ancient human remains are increasingly subjected to DNA analysis to gain knowledge about human prehistory. Commercial genetic ancestry tests are marketed widely as a way of discovering our personal evolutionary roots. Nation-states have established their own genetic projects to identify molecular-level variation within the national population. A growing number of biobanks are being launched to facilitate the development of what is hoped to become personalized medicine. Pharmaceutical drugs are marketed to particular racialized groups based on the assumption that populations respond differently to pharmaceutical substances. Criminal investigations are using DNA in the hope of identifying the ethnic background of the suspect who left their DNA at the crime scene. These diverse population genetic practices shape human lives and societies on manifold levels, including personal, communal, institutional, economic, national, and transnational spheres of social organization and existence.

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What is particularly striking about these biotechnological practices is the multiple ways in which they invoke emotions or become entangled with political questions. For example, the use of forensic DNA analysis and forensic genetic databases in criminal investigation may support a politics of surveillance and fear; commercial genetic ancestry tests may generate powerful emotional experiences of rootedness and exciting discovery; and the genetic analysis of ancient human remains may appear as serving a shared need to trace the footsteps of early humans, and thus as ideologically neutral. How does population genetics yield such a range of biotechnological practices? How can it be mobilized to enact mutually conflicting social, cultural, and epistemic projects? Why does population genetics become integrated so easily into mutually contradictory narratives of belonging, and why tensions between those narratives seldom attract attention?

My book addresses these questions in the context of *nonmedical population genetics*, that is, population genetic research and practices that seek to understand human evolutionary ancestry. The book focuses on an issue at the heart of nonmedical population genetics: *belonging*. Population genetics is about establishing connection between modern humans and prehistoric populations. By tracing the inheritance and gradual mutation of ancestral molecular structures—particular mitochondrial or Y-chromosome haplogroups, for example—population genetics seeks to locate geographic sites of origins, foundational moments of prehistoric migration, or events that led to the divergence of human populations. In doing so, population genetics produces roots, ties, and belonging. Furthermore, population genetics is about measuring variation among modern populations. By identifying, for example, single nucleotide polymorphisms (SNPs; pronounced "snips")—that is, specific loci in the human genome where people vary—population genetics seeks to place modern human populations within the wider patterns of human evolution. While we all belong to the rest of the natural world through our genetic roots, modern human populations *belong differently* to specific geographic sites or evolutionary landscapes. Likewise, some populations emerge as more closely connected to one another than others. Seen from this vantage point, population genetics produces *temporally and geographically organized webs of belonging*. Yet, as the range of practices drawing on population genetics demonstrates, this web of belonging is ontologically

multiple in that it is *enacted* differently (Mol 2002) at various cultural and technoscientific sites.

Population Genetics and Belonging interrogates this organizing ambiguity of population genetic belonging. The book argues that analyzing this ambiguity is pivotal to understanding how population genetics is shaping belonging and our ways of relating to each other. Science studies and critical social studies literature has explored extensively the ways in which population genetic practices may shore up problematic assumptions about racial differences (e.g. Hinterberger 2012; Koenig et al. 2008; Reardon 2005; TallBear 2013; Wailoo et al. 2012; Wald 2006; Whitmarsh and Jones 2010). While some scholars locate conservative politics in societal applications of population genetics, such as the use of forensic DNA in criminal investigation, others have argued that population geneticists' way of conceptualizing variation through geographically localized populations is in itself inseparable from the idea of distinct, biologically grounded races. These critical analyses have provided analytically insightful and culturally important ways of evaluating the role of population genetics in society, and they inform my discussions throughout the book. However, I approach the connection between population genetics and politics from a somewhat different angle: I highlight the ambivalence of population genetics as a tool for political and cultural projects. Both population genetic research and its societal applications are ontologically blurry and affectively manifold, with the result that population genetics can be invoked to support mutually contradictory political and cultural imaginaries. Indeed, this affective and epistemic ambiguity is precisely why population genetics resonates so widely across culture and society. In the chapters that follow, I trace the ways in which population genetics simultaneously both expands and curtails the ways in which belonging can be imagined and enacted in technoscientific societies.

Situating the Book

Population genetic projects emerged as objects of extensive critical analysis especially in the early years of the new millennium. This scholarly interest arose largely from the public debates in the 1990s surrounding

the Human Genome Diversity Project—the "sister project" of the Human Genome Project—that intended to turn the scientific attention from human sameness to variation. Jenny Reardon's book *Race to the Finish: Identity and Governance in an Age of Genomics* and Amade M'charek's book *The Human Genome Diversity Project: An Ethnography of Scientific Practice*, both published in 2005, were groundbreaking in their detailed explorations of the Human Genome Diversity Project. Reardon and M'charek both interrogate the complex entanglement of *population* and *race* in population genetic research on human diversity. While Reardon explores the underlying politics of the Human Genome Diversity Project through public debates, policies, statements, and practices, M'charek investigates how population genetic knowledges are produced in the lab.

In the past few years, when my book was already far along in the process of becoming a book-length manuscript, several new books on population genetics have appeared. Kim TallBear's *Native American DNA: Tribal Belonging and the False Promise of Genetic Science* (2013) examines how population genetics has sought to define Native American genetic ancestry. TallBear evaluates critically the implications of population genetic research and its commercialized applications for Native American communities, emphasizing the incompatibility of the idea of genetic belonging and Native American concepts of belonging. Alondra Nelson's *The Social Life of DNA: Race, Reparations, and Reconciliation after the Genome* (2016) explores how African Americans have embraced population genetic technologies such as genetic ancestry tests to establish roots in Africa beyond the devastating history of slavery, and how they use those roots to their own personal and communal ends. Focusing on social and communal practices, Nelson's study makes visible the often-creative ways in which members of communities invoke and appropriate population genetic technologies. Marianne Sommer's *History Within: The Science, Culture, and Politics of Bones, Organisms, and Molecules* (2016) situates the work of the famous population geneticist Luigi Luca Cavalli-Sforza within the history of evolutionary biology in the long twentieth century. Through the metaphor of "history within," Sommer identifies patterns and shifts between population genetics and earlier scientific approaches to how organisms embody past evolutionary history. Catherine Nash's *Genetic Geographies: The Trouble with Ancestry* (2015)

interrogates how population genetics has naturalized ideas of racial, national, and sexual difference. Building on cultural geography, Nash analyzes how relatedness is produced through the interplay of ideas of shared and unique ancestry. My book resonates with all of these works, but especially with Nash's book. Yet our approaches differ in crucial ways. While Nash approaches population genetics through the analytical lens of geographic space, I approach it through the analytical lens of temporality. While space and time are entangled in evolutionary processes (see Oikkonen 2015), the spatial and temporal lenses make visible different aspects of how population genetics is shaping belonging.

Population Genetics and Belonging focuses on processes of change through which population genetics becomes naturalized as an epistemically privileged way of understanding ancestry and kinship in a range of cultural practices. In order to capture such processes, the book seeks to identify gradual shifts, abrupt changes, persistent patterns, as well as underlying continuities in how roots and relatedness are imagined and enacted from the late 1980s until recent years. However, the book is not a history of population genetics. I approach transformations through selected case studies rather than a systematic historical approach. The case studies center on affective, narrative, and technological shifts that have molded cultural ideas and social categories of belonging. In this, *Population Genetics and Belonging* builds on and develops further the analysis of narrative transformation that I engaged in in my previous book *Gender, Sexuality and Reproduction in Evolutionary Narratives* (2013). The book traced the links between contemporary evolutionary narratives—especially those generated by evolutionary psychology—and the Darwinian narrative tradition, and investigated the evolving connections between narrative form, assumptions of gender and sexuality, and the affective of appeal of evolutionary explanations.

In terms of methodology, *Population Genetics and Belonging* brings together two types of inquiry that, in my experience, seldom meet: detailed examination of technologies and cultural analysis of affective and narrative investments. The first type of inquiry is part of the analytical repertoire of science and technology studies. Science and technology studies scholars question the assumption that scientific fields and their technological practices are monolithic. There is no such thing as a single

"population genetics" but rather a range of practices and technologies that often (but not always) fall under that label. These practices and technologies in turn have different material and discursive effects in particular historical and transnational settings. This makes the question of the relationship between science and politics situated, local, and performed rather than something that cuts through an entire field of science. Amade M'charek's book *The Human Genome Diversity Project* (2005) has been particularly important for me in thinking through these questions, as it has helped me untangle the *situatedness* of population genetic knowledge production and its effects on culturally salient categories such as race, gender, sexuality, or belonging. As M'charek shows, what population or variation is in specific situated practices depends on material and epistemic factors such as the availability and choice of biological samples, cell lines, reference genomes, genetic databases, methodological premises, and computer programs, as well as advances in sequencing technologies.

I want to combine science and technology studies analysis of situated biotechnological practices with cultural analysis of affective intensities and narrative dynamics. As much as I enjoy the richness and insights of science studies analyses of technological practices and their outcomes, such analyses seldom engage in in-depth analysis of how science operates in culture. While there are plenty of perceptive explorations of how science is represented in cultural products or received by publics, my focus is on the *underlying dynamics* that organize where and how scientific knowledge becomes integrated into cultural imaginaries, vocabularies, and narratives. It is my contention that such dynamics involves affective intensities, circulation of emotions, temporal investments such as nostalgia or longing, the structural pull of narrative toward futurity, and assumptions of reproduction as a symbolic promise of continuity. Crucially, these phenomena are largely intangible, becoming discernible only when traced through a range of texts, genres, and cultural sites. I believe that we need to pay careful attention to these issues in order to understand the intricate ways in which population genetics is molding the preconditions of our embodied personal and communal existence.

While *Population Genetics and Belonging* is not primarily a methodological work, it outlines and develops an approach that brings together the specificity and materiality of biotechnological practices and cultural

theorization of affect, temporality, and difference. This conjoiner of approaches does not come without compromise. For example, the specificity of biotechnological practices operates in the book on the level of three general approaches to genetic ancestry: *mitochondrial analysis*, which traces exclusively maternal ancestry; *Y-chromosome analysis*, which traces exclusively paternal ancestry; and *genome-wide analysis*, which traces genetic variation along the genome inherited (mostly) from both parents.[1] Each of these approaches includes in fact a number of methods and technological maneuvers; to give an example, while admixture studies and genome-wide association studies analyze genome-wide variation, they conceptualize variation and ancestry differently (Fujimura et al. 2010). Whereas an ethnographer of scientific practice would likely zoom into one of these micro-level practices of knowledge production, my focus is on how population genetics operates at the intersection of science and culture. For that reason, I examine population genetic technologies in terms of the three more general approaches to genetic material: mitochondrial, Y-chromosome, and genome-wide analysis. When population genetics enters cultural discourses and imaginaries, it rarely operates on a level that would be more detailed than these three approaches—in fact, even the presence of these three ways of approaching genetic ancestry is often implicit rather than explicit. One of the goals of my analysis is to make visible the technological underpinnings of cultural discourse on belonging on the level of these three approaches.

The chapters that follow foreground moments and sites at which these three approaches appear as distinct from one another, on the one hand, and seem to merge into each other, on the other. For example, Chap. 2 shows how Y-chromosome analysis of human ancestry appeared as both opposite and parallel to mitochondrial analysis in the 1990s. Chapter 3 identifies a technological shift and a rhetorical juxtaposition between mitochondrial and genome-wide techniques in ancient DNA research. Furthermore, in studies of genetic variation within nations explored in Chap. 5, mitochondrial and Y-chromosome analyses become sometimes conceived as one approach focusing on *uniparental* genetic ancestry (genetic inheritance through a single line of parents), which is contrasted with *autosomal* analysis (genome-wide research focusing on the chromosomes inherited from both parents, that is, all chromosomes except X and

Y). I trace how differences and similarities between mitochondrial, Y-chromosome, and genome-wide approaches are produced at particular moments in the history of population genetics, such as the introduction of high-throughput sequencing in the first decade of the twenty-first century, or in particular cultural applications, such as commercial genetic ancestry tests. I suggest that these various configurations of mitochondrial, Y-chromosome, and genome-wide technologies take shape through cultural imaginaries and affective investments. At the same time, they also shape the affective, narrative, and epistemic frameworks through which population genetic knowledge operates in culture.

On Population Genetics

Population genetics emerged from the so-called *modern synthesis* in the early twentieth century. The modern evolutionary synthesis brought together Charles Darwin's theory of natural selection and the role of environment and competition in the evolution of species, and Gregor Mendel's observations about the inheritance of characteristics based on his experiments with peas. Historical accounts of the emergence of population genetics typically identify three figures who laid the foundations of the field in the period between the two world wars: Ronald Fisher, J. B. S. Haldane, and Sewall Wright. From the very beginning, population genetics has drawn heavily on statistics and mathematical models. During the second half of the twentieth century, empirical evidence derived from testing and manipulating molecular material has become increasingly central to population genetic knowledge production. Nevertheless, statistical models remain in the heart of population genetics. For example, the idea of "molecular clock"—the use of harmless mutations in DNA to evaluate the evolutionary distance between populations—relies on complex statistical models and requires the use of computer programs that generate evolutionary trees of relatedness.

My study of population genetics and belonging begins with the introduction of mitochondrial analysis of human variation in the 1980s. It follows the scientific and cultural debate that surrounded the use of human mitochondrial DNA (mtDNA) to trace human evolution to pre-

historic Africa and to evaluate the evolutionary distance between world populations on the basis of mitochondrial mutations. In the mid-1990s, mitochondrial ancestries were increasingly supplemented and sometimes replaced by Y-chromosome ancestries, a key shift whose implications I trace in Chap. 2. I also examine how the idea of mitochondrial ancestry was adopted to study ancient DNA and thereby produce knowledge about relatedness that paleontological methods of studying fossilized bones could allegedly not engender. The perceived role of both mitochondrial and Y-chromosome analyses as tools of discovering ancestry has changed considerably after the introduction of new sequencing technologies in the past 15 years. However, as the following chapters will show, these shifts are not straightforward in terms of their affective investments or narrative framing. Instead, they take multiple forms and accrue various meanings at different sites and in different population genetic practices.

In the past two decades in particular, a significant strand of population genetic research has emerged around the connection between populations and diseases. This biomedical research draws on population genetic studies of population-level differences while connecting that information to genes that cause, control, or increase susceptibility to certain diseases. As mentioned at the beginning of this chapter, my main focus is not on this biomedical research, but on *nonmedical* population genetics. Nonmedical population genetics interrogates population-level variation in order to understand how human genetic diversity has evolved. Until the new millennium, the research focused often on *noncoding* genetic material, that is, genetic material that does not directly control physiological or behavioral characteristics and therefore was not considered to have biomedical significance. With the development and growing financial feasibility of genome-wide sequencing technologies in the past decade, the gap between biomedical and nonmedical population genetics has narrowed. As several scholars have observed, questions of genetic ancestry have become increasingly entangled with the molecular governance of health, illness, and risk (Rose 2008; Smart et al. 2017). While my book focuses on nonmedical research on genetic ancestry and the evolution of human genetic diversity from the late 1980s until the 2010s, the biomedical interest in population-level variation in disease inheritance

constitutes a parallel and interconnected history that becomes occasionally visible, as in the connection between the perceived genetic uniqueness of Finns within Europe and the idea of Finnish disease heritage in Chap. 5.

I approach population genetics as a phenomenon that spans from institutional science to public discourse and policies to popular culture. That is, instead of conceptualizing population genetics through a boundary between science and its societal applications, I view population genetics as an evolving set of technological, material, narrative, and affective practices that range from the molecular genetics lab to commercial biotechnologies to science journalism and fiction to public debates about immigration and national roots. This involves highlighting how realms of knowledge production and circulation are interconnected and overlapping. For example, as science communication scholars have long recognized, there is no clear boundary between science and its popularization, or even science and popular culture. Such boundaries are constructed retrospectively, they need to be maintained through repetition, and they may be politically charged (e.g. Gieryn 1999; Hilgartner 1990; Oikkonen 2013; Wald 2000). In the chapters that follow, I trace transformations of belonging *across* various genres, practices, technologies, discourses, narratives, and imaginaries that have emerged around evolutionary ancestry and human genetic diversity.

On Culture

The book traces population genetics and belonging in the context of culture. As culture is a notably fuzzy phenomenon, a few words on what is meant by *culture* may be useful. I approach culture as a *dynamic* that underlies the relations, activities, and institutions that constitute society. Culture may manifest itself in cultural products (films, novels, popular culture), practices (public celebrations, expected behavior), representations (symbols, repeated ways of portraying certain issues), or institutions (universities, museums, daycare centers). But culture may also remain in the background: it is the organizing logic that makes these artifacts, practices, representations, and institutions appear as meaningful and neces-

sary. Culture makes some things appear as natural while making others anomalies: for example, sexual arrangements or ways of organizing family relations are often rendered "normal" or "unnatural" through cultural norms and expectations. Culture is also situated: there are localized professional, regional, socioeconomic, ethnic, or gendered cultures. Yet culture also cuts across these realms producing repeated patterns that shape values and meanings at different sites and connects the sites into larger frameworks, such as nations.

My analysis focuses on three aspects of culture. First, I examine culture through *narratives*. Put briefly, narrative is the arrangement of events into a coherent sequence. Narrative gives the events a sense of likelihood or inherent motivation that suggests that the end of the narrative results from the earlier events, and yet the end is something more than the mere list of events. Judith Roof (1996) has argued that narratives are organized on a logic of production that generates something new, such as value, knowledge, movement, or a heterosexual union. This production of new operates itself as a promise of the continuation of narrative. Narrative has also an epistemic function: the productive logic of narrative generates accounts of the world that appear as logical or necessary. In my analysis of population genetics, I view narrative as a dynamic through which culture operates, and through which particular technoscientific formations appear as necessary or desirable. Narratives may be collective or institutional, as in national narratives, evolutionary narratives, or narratives of progress around biotechnological developments. Narratives may also be intimate or social, as in narratives of marriage, migration, or discovery of roots through genetic ancestry tests. Significantly, these collective and personal narratives are organized on an underlying dynamic that engenders a sense of movement. I am interested in narrative because it enables us to examine the resonances and tensions that arise when the structural tendencies of narrative—the "pull" of narrative, the sense that narrative needs to produce movement—takes new shapes at particular sites of technoscientific culture.[2]

Second, I explore population genetics and belonging through *cultural vocabularies*. By vocabularies I mean sets of phrases, words, metaphors, and other linguistic or visual elements that often appear together. Vocabularies are discursive phenomena, and in the chapters that follow I

sometimes use *vocabularies* and *discourses* interchangeably. However, I understand vocabularies as somewhat more narrow and specific than discourse in its general, often untheorized usage. As the plural form suggests, vocabularies are multiple at any given time, and accounts of scientific advance, for example, often employ various cultural vocabularies. Moreover, I use the term vocabularies to highlight how linguistic and visual elements operate as rhetorical *resources* in cultural accounts of biotechnological change.

Third, I investigate population genetics and belonging through *cultural imaginaries*. This concept has obvious resonances with the concept of *sociotechnical imaginaries* (Jasanoff and Kim 2009, 2015). Sociotechnical imaginaries refers to the ways in which views of scientific or technological progress are implicated in visions about communal futures or collective good, and how such visions shape technoscientific change. Similarly, my use of cultural imaginaries seeks to show, for example, how cultural ideas of future-oriented temporality affect how population genetic technologies become charged with affect. While cultural imaginaries and sociotechnical imaginaries overlap, the idea of cultural imaginaries foregrounds connections between science and popular culture, variations of narrative across genres, cultural circulation of affective intensities, or emotional underpinnings of temporality. Cultural imaginaries also emphasize how the ways in which science is made sense of in culture are connected to the conventions of literary narration or visual representation. These connections become visible in my reading of population genetics and belonging through works of fiction in Chaps. 2 and 4.

Narratives, vocabularies, and imaginaries are mutually entangled. Narratives employ vocabularies and draw from cultural imaginaries. Narratives may also add to cultural vocabularies, and may challenge or reinforce cultural imaginaries. Vocabularies often reflect cultural imaginaries. Cultural imaginaries, in turn, draw on collective narratives, such as national narratives, but may also shape those narratives. These three aspects of culture, then, are ultimately inseparable. However, looking at culture through each of these concepts renders visible slightly different aspects of population genetic belonging. Used together, they help shed light on the underlying dynamic that organizes the role of population genetics in culture.

On Belonging

Belonging has emerged as a central concept in social and cultural research. Researchers have approached belonging as a set of emotional, psychological, as well as political ties between people and communities (e.g. Anthias 2009; Antonsich 2010; Yuval-Davis; 2011). Belonging has often replaced the concept of identity (see Lähdesmäki et al. 2016), which points to the embeddedness of belonging in questions of personal and communal experience. Belonging has been a particularly fruitful way of analyzing the construction of identities and experiences in relation to communal boundaries, national borders, and practices of exclusion especially in the context of postcolonial and migration studies (e.g. Christensen 2009; Fortier 2000; Yuval-Davis 2011). Furthermore, belonging is often approached through space as a person's or community's belonging (or longing to belong) to a particular real or imaginary place.

My book approaches belonging from a somewhat different angle. First, I approach belonging as a *temporal dynamic*. This temporal dynamic engenders affectively resonant connections between the past, present, and future, anchoring individuals and communities in culturally meaningful historical processes. Temporality is particularly important to population genetics as evolution is a way of organizing the past, present, and future into a forward-moving narrative (Oikkonen 2013). In the following chapters, I show how population genetics has refashioned belonging by redefining the link between *origins* and *futurity* (the temporality of belonging), and the idea of *community* (the network of emerging relations that one belongs to) in evolutionary terms. At the same time, I emphasize that belonging is ontologically ambiguous and multiple. This multiplicity arises from the ways in which different population genetic technologies, such as mitochondrial, Y-chromosome, and genome-wide analyses, produce patterns of difference and sameness, and locate them within the temporal dynamics of human evolution. Second, I focus on affective shifts and narrative transformations that organize how belonging may be imagined and enacted. I do not study people or communities, or their emotional experiences and social ties. Instead, I examine

technologies, vocabularies, and imaginaries that make particular forms of belonging desirable, likely or inconceivable in contemporary technoscientific societies.

Throughout the book, I approach the temporal dynamic of belonging as entangled with intersectional differences and affective investments. By *intersectionality*, I refer to how categories of difference such as race, gender, sexuality, class, or age take shape through one another in technoscientific practices (M'charek 2010; Schiebinger [1993] 2004). For example, as I argue in Chap. 2, the idea of a molecular connection between modern humans and prehistoric populations that emerged from the study of mitochondrial ancestry in the late 1980s became framed through a changing configuration of gender, sexuality, and race throughout the 1990s. This was not a matter of one category of difference replacing another, but implicated in each were assumptions of other differences, with the result that gender was racialized and race heterosexualized. Furthermore, categories of difference do not have a fixed meaning. What is race or gender in a particular technological or cultural situation is always an open question. Nevertheless, categories of difference carry traces of their previous uses, which shape the kinds of effects they will have in the new settings.

The book shows that population genetic belonging engenders and organizes affect. I approach affect as movement of emotional intensities and investments at the intersection of sites, genres, and technological practices. Instead of drawing a clear line between prediscursive *affect* and culturally nameable *emotion*, I focus on technoscientific formations in which affective intensities, such as a sense of forward-moving time, and cultural emotions, such as the narrative framing of objects, are mutually entangled. For this reason, I use affect and emotion largely interchangeably. Furthermore, drawing on Sara Ahmed's (2004) work, I trace how technoscientific objects become emotionally charged, and how affective intensities and cultural emotions travel across sites. My analysis is also influenced by Sarah Franklin's (2007) genealogical approach to shifts and continuities in the affective investments underlying how biotechnologies are envisioned, developed, and naturalized. Through her analysis of the cloning of Dolly the sheep, Franklin shows how affective histories of technologies shape scientific futures. What makes affect so central to

population genetics is that the temporality of evolution itself is affectively charged through its promise to connect us to roots as well as to futurity. In Chap. 4, I introduce and develop the concept of *evolutionary nostalgia* to capture how evolutionary narratives operate on a sense of longing that connects us to a prehistoric past in order to imagine and enact an alternative present and a better future. My reading of this two-way affective temporality challenges the common perception that population genetic forms of belonging are past-oriented.

Affective investments and intersectional differences are entangled in multiple and intricate ways in the forms of belonging that population genetics generates. My analysis of these entanglements draws on Amade M'charek, Katharina Schramm, and David Skinner's (2014) *topological understanding of race*. M'charek, Schramm, and Skinner show how race appears, disappears, and takes different forms at the intersection of specific practices, for example, when different systems of surveillance and biotechnological monitoring are brought together. In other words, race is situated and technologically enacted, which is why it escapes so easily attempts to identify its presence in laws or policies. I extend the idea of topology to the culturally and historically situated formations of affect, temporality, and difference that I trace. I view these formations of affect and intersectional differences as *enacted* through specific and situated conjoiners of technological practice, epistemic claims, and cultural frameworks. In these situated constellations, certain differences and tendencies become foregrounded, while others disappear to the background. Crucially, this means that a different way of framing and contextualizing the studied phenomena—population genetics and belonging—would have rendered visible different formations of affect and differences.

Materials

The book explores how population genetics has shaped belonging through case studies, encompassing the debate about Mitochondrial Eve, the uses of DNA retrieved from two ancient human remains, Kennewick Man and Cheddar Man, commercial genetic ancestry tests, the construction of national populations, as well as ongoing debates about immigration and

multiculturalism. The case studies were not selected in any systematic manner. I have chosen them because they elucidate several central aspects of how population genetics is changing our twenty-first-century lives. I also wanted to explore cases that have not been addressed extensively by others or have been analyzed from a different angle. The debate surrounding Mitochondrial Eve drew my attention when I was still finishing my previous book, and it became eventually the starting point for the current work. The legal controversy about the North American ancient human remains known as Kennewick Man was the second case I engaged in, as it seemed to capture something essential about the problematic relationship between population genetics and national narratives. The rest of the cases grew around these two initial case studies. The publically celebrated analysis of the mtDNA of Cheddar Man, the ancient human remains discovered in Somerset in the United Kingdom, appeared a logical point of comparison to the Kennewick debate. While commercial genetic ancestry tests have been among my research interests for several years, the overall argument and theoretical framework of the book made visible new aspects of the phenomenon. When I started the book, I did not intend to discuss national biobanks or the role of population genetics in immigration debates, but toward the end of the project they seemed increasingly important for my discussion of population genetic communities.

Each of the case studies draws on a range of genres. The chapters include media texts from newspaper headlines to science journalism, popular science books, articles in popular science magazines, websites of genetic ancestry testing companies, and articles published in scientific journals. I also read three novels and one short story, as they enable me to develop key aspects of the argument. The breadth of genres makes it possible to trace shifts, patterns, resonances, and tensions across science and society. This is pivotal for my project, as the object of my study is a largely intangible phenomenon—belonging—that cannot be pinned down to any genre or discursive formation. The array of genres also helps shed light on moments of unease or ambivalence when technoscientific objects, practices, or narratives travel across scientific, public, and popular genres.

Structure of the Book

Population Genetics and Belonging argues that population genetics engenders forms of belonging that are multiple and ambiguous, and that the cultural appeal of population genetics arises largely from this multiplicity and ambiguity. The book develops this argument through five chapters. Chapter 2, "Mitochondrial Eve and the Affective Politics of Scientific Technologies," traces the emergence and transformations of mitochondrial and Y-chromosome analyses. It focuses on the scientific and cultural debate that surrounded the figures of Mitochondrial Eve (the most recent matrilineal ancestor of currently living humans) and Y-chromosome Adam (the most recent patrilineal ancestor of currently living men) from 1987 through the 1990s. The chapter explores the affective engagements of these technologies, and especially the ways in which they emerged through, and were entangled in, racialized, gendered, and sexualized differences. I elaborate on these intersectional and affective entanglements through two works of fiction, Greg Egan's short story "Mitochondrial Eve" and Hideaki Sena's horror novel *Parasite Eve*.

Chapter 3, "Imagining Origins through Ancient Human DNA," explores how studies comparing modern DNA to DNA retrieved from ancient human remains engender a molecularized temporal trajectory that connects the bodies of modern humans to a fantasized point of origins in the prehistoric past. The chapter focuses on the debates surrounding two 9000-year-old human remains, the so-called Kennewick Man and Cheddar Man. In the Kennewick case, I trace how the heated cultural battle between scientists, local Native Americans, and a neo-Norse pagan cult evoked the idea of an embodied continuum of human generations in multiple ways, thus reinforcing mutually contradictory national, racial, and global narratives of belonging. In the Cheddar case, I show how a study claiming to connect Cheddar Man's mtDNA to a local schoolteacher became embedded in competing narratives of personal, regional, and national belonging, which in turn took shape through affectively charged ideas of masculinity and class. While identifying differences between American and British negotiations over origins, I also consider the implications of the shared assumption that the past resides inside the cells of modern people.

Chapter 4, "Evolutionary Nostalgia and the Temporality of Belonging," takes a closer look at the temporal dynamic that underlies the forms of belonging produced through the comparative study of ancient and modern DNA. I theorize this temporality through two novels: Kathleen O'Neal Gear and W. Michael Gear's popular prehistoric romance *People of the Raven*, which imagines the life of Kennewick Man, and Margaret Drabble's novel *The Peppered Moth*, which tells the story of three generations of mothers and daughters in the context of a mitochondrial analysis of ancient human remains very similar to the Cheddar case. I develop the concept of *evolutionary nostalgia* to capture the two-way temporal longing that organizes population genetic belonging and renders the imagined past the location of futurity. Building on scholarship on queer time, genetic temporality, and collective memory, the chapter explores the conceptual and material complexities of how pasts and futures are seen as unfolding from genetic analysis. The chapter also reflects on the role of genetic technologies—especially mitochondrial analysis evoked in Drabble's novel—in generating particular versions of evolutionary nostalgia.

Chapter 5, "Genetic Communities and the Boundaries of Belonging," asks what kinds of communities emerge from the temporal dynamics of population genetic belonging. The chapter theorizes and problematizes the connection between *population* and *community*. It examines the different ways in which the ambiguous connection between population and community is mobilized in commercial genetic ancestry tests, European evolutionary history, the idea of unique Finnish genetic inheritance, and public debates about immigration and multiculturalism. The chapter shows how the boundaries between region, nation, and continent are products of technological practice, including adjustments of evolutionary temporality, and how different population genetic practices produce changing patterns of difference and sameness. The chapter concludes with a discussion of the ambivalent connection between politics and population genetic belonging.

Chapter 6, "Reflections on Methodology and Biotechnological Change," elaborates on the book's empirical, methodological, and theoretical contribution. The chapter identifies and discusses larger patterns of continuity and transformation underlying the cases studied in the pre-

vious chapters. The chapter also discusses the usefulness of the methodological approach in the study of processes of biotechnological change.

Notes

1. Genome-wide analysis may also include the Y chromosome (but not mitochondria, which have their own mitochondrial genome). Genome-wide analysis that excludes the Y and X chromosomes is called "autosomal analysis."
2. For further discussion of narrative, see Oikkonen (2013).

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2

Mitochondrial Eve and the Affective Politics of Scientific Technologies

In the late 1990s, Iceland became the site of a heated debate about emerging uses of population genetic technologies. The debate concerned the construction of a national biobank, Icelandic Health Sector Database, which was to combine personal health records, genealogy information, and tissue samples from Icelandic citizens, and was to be carried out by a private company called deCODE. What made the suggested database so special was its attempt to cover the entire population of a nation. Iceland was widely seen as particularly suitable for such an endeavor: with only 275,000 inhabitants and surrounded by an ocean, the national population was assumed to be largely genetically homogenous. Moreover, Iceland's public health care system and extensive genealogy records provided unique insights into the health and history of the population.

While politicians, citizens and bioethicists debated the Icelandic database, another island—Ireland—emerged as an object of population genetic interest. The genetic composition of the Irish people was seen by many scientists as an interesting case study that could answer unresolved questions about the early history of Western Europe. This research differed from the developments in Iceland in several ways. Instead of seeking to establish a comprehensive database, population genetic research on

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Ireland took place mostly through academic projects, several of which were funded by the Royal Irish Academy's "Irish Origins" program. Furthermore, while the Icelandic database was connected to health-related issues and prospective pharmaceutical applications, population genetic studies of Irish ancestry often hoped to clarify the wider picture of the peopling of Europe.[1]

Although the two biotechnological endeavors were situated differently in relation to biomedicine, public health, and pharmaceutical industry, they shared crucial characteristics. They both built on the premise that the modern populations of the two islands carry in their cells concrete evidence of the ties that connect contemporary communities into a meaningful history of human evolution. They assumed that the modern people of the islands represented coherent, homogenous, prehistoric nations—at least to an extent that would be significant for population genetic and biomedical research. The two enterprises also mobilized ideas of individual ties that connected modern citizens to prehistoric ancestors as well as to their fellow citizens through specific molecular structures. Both endeavors, then, were entangled with ideas of not only national but also personal and communal belonging.

The Icelandic and Irish projects deployed similar genetic technologies, most importantly mitochondrial and Y-chromosome analyses. Mitochondrial analysis aims to trace maternal ancestry through mitochondrial DNA (mtDNA) inherited from the mother, whereas Y-chromosome analysis seeks to reconstruct paternal ancestry through Y-chromosome DNA passed from father to son. While the Icelandic and Irish projects can by no means be reduced to these two technologies, mitochondrial and Y-chromosome analyses provided key tools by which the genetic place of the Icelandic and Irish populations was to be outlined on the global map of human evolution. For example, in an article by deCODE and Oxford University scientists, Icelandic mtDNA was compared to Scandinavian, British, and other European mitochondrial sequences (Helgason et al. 2000), and in a 2003 follow-up study, the genetic composition of the Icelandic population was used to estimate the mutation rate of mitochondrial and Y-chromosome DNA (Helgason et al. 2003). Similarly, many of the Irish studies focused on Y-chromosomes. Researchers suggested, for example, that a large number of Irish men

with Gaelic last names, especially those living in the west of Ireland, have Y-chromosomes that are closely related and presumably originate from the same wave of prehistoric migration (Hill et al. 2000). Another study identified a specific version of this "Irish modal haplotype" shared by roughly one in five men in northwestern Ireland, while arguing that such genetic prominence may reflect the long-standing political and sexual dominance of the men of the Uí Néill family associated with the prehistoric king Niall of the Nine Hostages (Moore et al. 2006).

I do not intend to engage in an extensive analysis of the Irish and Icelandic cases here; that task has been taken up by a number of researchers, who have provided insightful comments on the two enterprises.[2] For the purposes of the current chapter, I invoke the two cases because they exemplify a particular transition in the history of population genetics. Ranging from the mid-1980s until the early years of the new millennium, this phase is characterized by the emergence of mitochondrial and Y-chromosome analyses, and their gradual establishment after initial years of controversy as standard tools in the study of human evolution. Toward the end of this period, mitochondrial and Y-chromosome DNA had emerged as primary means of accessing human past, and they were widely seen as promising unprecedented insights into the dynamic of belonging that connects people and communities across evolutionary time and global space. This routinization of mitochondrial and Y-chromosome technologies was instrumental in making national genetic enterprises such as the Icelandic biomedical database or the search for Irish genetic roots appear as scientifically and culturally meaningful.

The current chapter reaches beyond the Icelandic, Irish and other national projects into the underlying history of mitochondrial and Y-chromosome analyses. Focusing on the connections between technological development and changing forms of belonging, I trace the processes through which mitochondrial and Y-chromosome technologies have become entangled with ideas of race, gender, and sexuality, and how those differences have shaped belonging. While I follow historical transitions, I also pay attention to the multiplicity of belonging—that is, how practices surrounding mitochondrial and Y-chromosome analyses enact belonging in multiple and often contradictory ways. My analysis highlights ambiguities embedded in these two technologies, suggesting that

population genetics was never tied to a singular form of belonging, but was plural and ambivalent from the very beginning. I show how current forms of genetic belonging emerge from a contingent history of scientific technologies, thus highlighting the inseparability of the scientific present from the scientific past. Through my reading of the histories of mitochondrial and Y-chromosome analyses, I ask why these technologies carry considerable cultural appeal even after the introduction of advanced research technologies such as high-throughput genome-wide sequencing.

The chapter focuses on the affective underpinnings of mitochondrial and Y-chromosome technologies. It suggests that the intersections of gender, race, and sexuality that organize the history of mitochondrial and Y-chromosome technologies are embedded in affective politics. That is, these technologies are part and parcel of a cultural dynamic that appeals to, and feeds into, a cultural repertoire of emotions. This entanglement of technology and emotions indicates that current forms of genetic belonging emerge from affective investments, tensions, and ambiguities surrounding mitochondrial and Y-chromosome technologies. My exploration centers on two cultural figures that became symbolic of the promises of mitochondrial and Y-chromosome analyses: Mitochondrial Eve and Y-Chromosome Adam, our most recent common maternal and paternal ancestors. I trace the emergence and travels of these two figures through the affective investments of scientific articles, popular science texts, newspaper reports, as well as fiction. My reading demonstrates that the cultural meanings of scientific technologies are always ambivalent and subject to ongoing negotiations. These negotiations, in turn, take place in both science and popular culture, and especially in the contested and fuzzy borderland between the two. This affective ambivalence of scientific technologies structures and orientates the forms of belonging that surround population genetics today.

Population Genetics and Molecular Evolution

Population genetics emerged from the so-called modern evolutionary synthesis that brought together Mendelian genetics and Darwinian evolution through the work of R. A. Fisher, Sewall Wright and J. B.

S. Haldane in the period between the two World Wars. The new field of population genetics drew heavily on mathematics and statistics. Building on the synthesis of Mendelism and Darwinism, population genetics merged the study of spontaneous mutations as a source of genetic differences within and between populations and biometrical analysis of the stabilization or wielding of such variation. During the first half of the twentieth century, theoretical population geneticists often emphasized the formative role of natural selection in evolution (Bachmann 2001).

The rise of molecular biology in the 1950s challenged this strong selectionism. Following the discovery of the DNA structure, molecular biologists showed that only a portion of the DNA in the cell nucleus actually codes for proteins. In fact, much of the genome consists of noncoding DNA that is unnecessary for the functioning of the organism (Bachmann 2001, 14). In the 1960s, developments in biochemistry demonstrated that there is considerable genetic variation within populations of a species; the most important development was enzyme electrophoresis, a technique that measures the response of biomolecules to a negative electric charge, thereby locating molecular variation (Bachmann 2001, 17). These discoveries became part of a debate between representatives of "classical theory" and "balance theory" of evolution. While the former emphasized the role of natural selection in weeding genetic variation, the latter considered genetic variance in a species as a factor that improved the fitness of a population, that is, it improved the likelihood of survival and successful reproduction (Bachmann 2001, 16; Suárez and Barahona 1996, 66).

In the late 1960s, these developments led to the *neutral theory of molecular evolution*, developed especially by Motoo Kimura (Kimura 1968, 1969; Kimura and Ohta 1971) and Jack Lester King and Thomas H. Jukes (King and Jukes 1969). The theory drew on a series of experiments in molecular biology and biochemistry by such scientists as Emile Zuckerkandl and Linus Pauling (Zuckerkandl and Pauling 1962), and Emanuel Margoliash and Emil L. Smith (Margoliash 1963; Smith and Margoliash 1964).[3] Building on this tradition, Kimura, King, and Jukes argued that a large amount of molecular variation is neither delete-

rious nor advantageous but neutral. The theory was interpreted widely as an "attack on the tacit belief that every detail of a living organism was shaped, possibly perfected, by selection" (Bachmann 2001, 17). While the debate about the relative input of mutations versus natural selection in evolutionary processes continued (Bachmann 2001, 18), experimental results led to the establishment of the neutrality of molecular variation as a so-called null hypothesis in evolution. In other words, it became the premise on which evolutionary models are built.

The neutral theory of molecular evolution had important consequences for the scientific understanding of evolutionary processes across species. First, it shifted attention to molecular processes taking place inside the cells of the organism and invisible to the naked eye. Second, it suggested that noncoding DNA was not just evolutionary "noise" but recorded evolutionary history, and thus it could be used as a tool in investigating evolutionary processes. Third, the neutrality theory suggested that there was a gap between organismal and molecular levels in the evolution of populations, as a large number of molecular changes in the noncoding sections of the genome had no direct effect on the physical or behavioral traits of the organisms that make up the population. These ideas were reflected in the theory of *molecular clock*. The molecular clock built on the neutrality theory along with Zuckerkandl and Pauling's (1962) and Margoliash's (1963) work on the rate of molecular evolution (Kumar 2005; Morgan 1998). The molecular clock was based on the observation that molecular-level changes record the passage of time and thus the distance between species or populations: the more mutations there are between two populations, the earlier in the past their evolutionary paths diverged. Conversely, a small number of mutations indicate recent divergence. The theory of molecular clock was given empirical evidence and developed further by researchers like Allan Wilson, Vincent Sarich, and Mary-Claire King (Sarich and Wilson 1967; King and Wilson 1975). These scientists sought to produce models through which molecular difference could be translated into evolutionary distance and thus into prehistoric genealogies.

In the late 1970s, scholars working on the molecular clock became increasingly interested in mtDNA as a source of evolutionary informa-

tion. Mitochondria are tiny organelles that provide energy to the cells of eukaryotic (multicellular) species. What makes mtDNA particularly attractive in the study of molecular evolution is its location in the cytoplasm outside the cell nucleus. While nuclear DNA—the genetic information stored in the chromosomes in the cell nucleus—is subject to the recombination of maternal and paternal DNA in reproduction, human mtDNA is inherited from the mother. For this reason, mitochondrial mutations accumulate faster and at a more predictable rate than nuclear mutations. Furthermore, mtDNA is relatively concise (16,000 base pairs in humans) compared to nuclear DNA (3 billion base pairs in human gametes), and is hence easier to work with than nuclear DNA. As with earlier studies of molecular evolution, researchers were particularly interested in noncoding sections of DNA, which were seen as largely unaffected by natural selection.

Much of the work on mtDNA as a molecular clock took place in Allan Wilson's lab at the University of California, Berkeley. A crucial step was the analysis of restriction enzyme digestion of mtDNA introduced to the lab by postdoctoral researcher Wesley Brown in the late 1970s. This generated key papers which demonstrated that the rate of mitochondrial mutations was considerably more rapid than that of nuclear mutations (Brown et al. 1979), and that mtDNA could be used to evaluate the evolutionary relationship between humans and different species of ape (Ferris et al. 1981). The lab also examined the evolution of modern human populations through the analysis of human mtDNA collected from placentas. While this study showed considerable variation among humans, the Berkeley researchers were not yet able to link variation to particular ethnic origins, or to construct reliable mitochondrial lineages within human evolutionary history (Ferris et al. 1980). With the introduction of increasingly sophisticated models of computer analysis, as well as technical advances in the sequencing of mtDNA, a molecular vision of the evolution of human populations gradually emerged. This process was aided by the sequencing of the human mitochondrial genome in 1981, which provided a reference point for the study of human mitochondrial variation (Anderson et al. 1981; M'charek 2005, 84–119).

The 1987 Mitochondrial Paper and Its Reception

The study of mitochondrial ancestry marks a particularly intense, innovative and tumultuous phase in the history of human population genetics. In many ways, this development culminated in the introduction of the figure of Mitochondrial Eve in the late 1980s. The figure of Eve, and the affective politics that surround it, is the focus of the rest of this chapter. The travels of Mitochondrial Eve across science and popular culture make a fascinating object for analysis, as they capture the processes through which abstract ideas of difference materialize in an imagined gendered, sexualized, and racialized body. Eve's cross-cultural travels thus shed light on some of the underlying tendencies that organize population genetics throughout its history. They also point to the developments through which the idea of human racial diversity recorded in molecular structures inside our bodies becomes gradually translated into assumptions of nationally, regionally, and personally defined differences. As a result, the idea of a shared human evolutionary trajectory that initially informed the study of molecular evolution and mitochondrial ancestry is increasingly paralleled with, and overshadowed by, national, communal, and personal evolutionary trajectories.

The figure of Mitochondrial Eve arose from the research conducted in Wilson's lab at Berkeley throughout the 1980s. In the late 1970s, Rebecca L. Cann—then a doctoral student working with Wilson—started collecting ethnically diverse placentas rich with mtDNA from maternity wards in the United States. By the beginning of the 1980s, researchers were seeking to create *phylogeny trees* (trees of evolutionary relatedness) with analytical techniques and computer programs such as neighbor joining, phylogenetic analysis using parsimony (PAUP), and Fitch-Margoliash method. These techniques were not, however, able to tease out networks of evolutionary differences between placental samples reliably at this stage, and thus mtDNA could not yet be translated into a conclusive and satisfactory model of human ancestry. In 1981, Mark Stoneking joined Wilson's lab as a then-graduate student. He set out to provide additional mitochondrial samples in order to expand and strengthen the mitochondrial model of human ancestry theorized by Wilson and colleagues. By 1985,

the samples used by the Berkeley scientists had versified in terms of ethnic origins, including now mtDNA also from aboriginal Australians and New Guineans collected by Stoneking.

Rebecca Cann, Mark Stoneking, and Allan Wilson's landmark paper, "Mitochondrial DNA and Human Evolution," was published in the prestigious science journal *Nature* in January 1987. The paper relied on the analysis of 145 geographically diverse placentas, as well as two cell lines—HeLa and GM 3043—representing, respectively, African American and aboriginal (!Kung) South African inheritance (Cann et al. 1987). Wilson's team used placentas because they are rich in DNA, a practical necessity in the early 1980s before the invention of polymerase chain reaction (PCR), the technique that enabled the multiplication of genetic material. Two-thirds of the placentas came from the hospitals in the United States, while the rest were collected in Australia and New Guinea. The authors emphasize that the samples included "representatives of 5 geographic regions: 20 Africans (representing the sub-Saharan region), 34 Asians (originating from China, Vietnam, Laos, the Philippines, Indonesia and Tonga), 46 Caucasians (originating from Europe, North Africa, and the Middle East), 21 aboriginal Australians, and 26 aboriginal New Guineans" (Cann et al. 1987, 32). However, only two of the African samples came from individuals born in Africa; the rest were collected from African Americans. Science studies scholar Amade M'charek (2005, 95–100) notes that Cann, Stoneking, and Wilson's paper relied on a logic of circulation and availability characteristic of laboratory science: the placentas had to be fresh and correctly transported, and the cell lines had to be among those available to the lab. Laboratory practices, then, are not necessarily based on the ideal choice of material. Rather, they participate in the processes through which particular tissues and techniques become naturalized as means of producing new knowledge. M'charek observes that the technological and material choices of Cann and colleagues' paper operate in the same fashion.

Cann, Stoneking, and Wilson used 12 restriction enzymes to identify *polymorphisms*, that is, genetic markers where individuals vary. These identified differences were then subjected to a computer analysis with the goal of building a phylogeny tree. On the basis of this analysis, Cann, Stoneking, and Wilson argue that "[i]n general, Africans are the most

diverse and Asians the next most, across all functional regions," which suggests that "Africa is a likely source of the human mitochondrial gene pool" (Cann et al. 1987, 33). Accordingly, the paper proposes an evolutionary tree that connects "maternal lineages in modern human populations to a common ancestral female (bearing mtDNA type a)" (Cann et al. 1987, 33). As many have pointed out, computer programs produce several alternative genealogy trees on the basis of a host of theoretical assumptions (Marks 2001; Bolnick 2008). Wilson's team chose a parsimony tree, the genealogy that relies on the fewest number of evolutionary changes. They also gave this tree a temporal scope, as their estimated mutation rate of 2–4% per million years "implies that the common ancestor of all surviving mtDNA types existed 140,000–290,000 years ago" (Cann et al. 1987, 34). This use of statistical models puts the ontological status of the mitochondrial ancestor in an ambivalent light. While today's mitochondrial lines must converge at a specific point in prehistory, the exact moment and location of that convergence is produced through the choice of method and material. In this sense, the historically specific female body from which all our mtDNA is derived is characterized by foundational ambiguity. This prehistoric point of convergence is a logical necessity arising from our understanding of evolutionary processes as gradual emergence of new evolutionary lineages. It is also a material fact in the sense that it is based on the mutations accumulated in our DNA. And yet it is a statistical inference in the sense that different techniques and computer programs would locate the point of most recent shared mitochondrial ancestry in a slightly different prehistorical moment and thus in a different gendered body.

Wilson's team's mitochondrial hypothesis, and the idea of molecular clock that underlay it, touched directly upon two heated scientific debates. The first debate centered on the question of where and when anatomically modern humans emerged. At the time there were two main competing theories, which each had supporters in both paleontology and population genetics. The *multiregional hypothesis* proposed that anatomically modern humans evolved in several different locations in Asia, Africa, and Europe at the beginning of the Pleistocene era some two million years ago (Wolpoff et al. 1988; Frayer et al. 1993, 1994; Templeton 1993, 1994). The *out-of-Africa hypothesis* maintained that anatomically modern

humans appeared in Africa a few hundred thousand years ago, and then migrated across other continents, eventually replacing other hominids (Stringer and Andrews 1988a, b; Vigilant et al. 1991; Stoneking 1993). The Berkeley scientists' mitochondrial hypothesis represented the latter approach. To complicate things further, Wilson's team's proposal also ran against earlier suggestions that Asia was a likely place of origin for modern humans (Denaro et al. 1981).

The second debate was the controversy between paleontology and population genetics over what should count as evidence in the study of human evolution. While many paleontologists considered fossil evidence as the epistemically privileged source of evolutionary knowledge, many geneticists saw molecular knowledge as the cutting edge that would finally lead the study of human evolution beyond the incomplete fossil record. This development is significant in that it refashioned the idea of material evidence: while fossils had been long seen as the material witnesses to the evolutionary past, proponents of genetic analysis sought to replace their significance with the materiality of DNA. Furthermore, the two debates were interconnected in crucial ways: the debate about the geographical origins of modern humanity was entangled with ideas of *proper* versus *false* genetic analysis, as suggested by the ardent criticism of the Mitochondrial Eve hypothesis by geneticist Alan Templeton (1993).

Emotions played a central role in the mitochondrial debate from the very beginning. In a 2010 interview for the journal *PLoS Genetics*, Rebecca Cann describes the tensions and outcries among scientists that followed the publication of the 1987 mitochondrial paper:

> I got a lot of hate mail, crank mail, some with strange scrawling notes. I even got a visit from the FBI after the Unabomber attacks. I got random calls in the middle of the night, and people on flight layovers wanted to talk. I was unprepared for this role as the molecular person questioning the fossils … It made me mad because people were doing the same thing with birds and lizards and fish and they weren't taking anywhere near the amount of crap I was taking. I could see it was only because I was talking about humans. These arguments raised so much emotion, and that really depressed me. (Gitschier 2010, 4)

This is, of course, a retrospective account by one involved individual, and should therefore not be read as an exhaustive description of the controversy. Nonetheless, it explicates how the issue of mitochondrial ancestry was construed as a deeply affective terrain from the outset. These emotional tensions become apparent in journal articles and scientific commentaries published in the late 1980s and early 1990s. For example, in a series of commentaries published in the journal *American Anthropologist*, scientists engaged in a heated exchange about the merits and weaknesses of mitochondrial theory. Critics of mitochondrial theory used emotionally charged phrases such as "dogmatic assertions" (Frayer et al. 1993, 36), "damaging contradictory data" (Templeton 1993, 69), and "attempts to shoehorn fossils into a discredited genetic framework they do not (and never did) match" (Frayer et al. 1993, 42). In an equally spirited tone, critics of multiregional theory referred to "double standards" (Stringer and Bräuer 1994, 422) and "the perils of ignoring or dismissing genetic evidence" (Stoneking 1994, 138). These quotes point to the entanglements between the two debates described above, as both fossils and genetic variation are invoked alternately as the epistemically privileged site of knowledge production about the prehistoric human past.

While these examples suggest that feelings of annoyance and alliance must have affected the involved parties intimately, my focus is not on such private feelings, but on the ways in which texts about science appropriate cultural logics of emotion. In particular, I am interested in how scientific technologies become entangled with changing cultural values and affective commitments, that is, how they gain their power to move emotions. I am also interested in the malleability of scientific technologies, that is, how technologies are invoked to enact multiple and mutually contradictory realities. Cann's interview and the *American Anthropologist* exchange indicate that despite the original framing of mitochondrial ancestry in terms of computational models and gene frequencies, the idea of an African mitochondrial ancestor resonated strongly among scientists. The figure of Eve, then, was embedded in affective politics from the very beginning. These affective negotiations concerned the epistemic status of DNA evidence, the point of origins for modern humanity—and, as we shall see, the role of gender, race, and sexuality in that history.

These affective negotiations took place through a range of genres, including research articles, science reviews, technical commentaries, as well as retrospective interviews, thereby highlighting the blurriness of the boundaries between scientific genres. Science studies scholars have argued that science does not enter culture through a straightforward path of popularization but through a two-way movement (Beer [1983] 2000; Hilgartner 1990; Terry 2000; Wald 2000, 2008). On the one hand, science becomes interwoven into cultural narratives, discourses, and metaphors that are being invoked in a range of cultural genres from popular science magazines and science news to film and fiction. On the other hand, these narratives, discourses, and metaphors shape the parameters within which scientific projects or research questions are conceived of as meaningful or important. What passes through textual borders in these processes of travel is not only argument or rhetoric, but also emotional investments and cultural values. As the following sections demonstrate, this circulation of affect in scientific texts and technologies is closely connected to the affective structures of news reporting as well as those of popular culture.

The Proto-Feminist Eve

While Cann, Stoneking, and Wilson's 1987 article avoided naming the inferred mitochondrial ancestor, this abstract point of genetic convergence became quickly known as "Mitochondrial Eve" or "African Eve" in the ensuing controversy.[4] With the emergence of Mitochondrial Eve, human difference as statistical variation largely disappears behind the image of a unique, original ancestral mother, thus marking a key shift in how genetic ancestry is imagined. Through this shift, the figure of Mitochondrial Eve joined the spare ranks of prehistoric female ancestors such as the three-million-year-old *Australopithecus afarensis* fossil "Lucy" found in Ethiopia in 1974 and named after the Beatles song "Lucy in the sky with diamonds." Yet Mitochondrial Eve differed from paleoanthropological female figures in crucial ways. Eve's figure embodied the cultural prestige and epistemic authority attached to new biotechnologies. Her figure also sug-

gested that population genetics was able to engender culturally relevant and emotionally powerful visions of the past instead of mere statistical estimates of genetic variation.

The name Eve was introduced in Jim Wainscoat's (1987) commentary published in the same *Nature* issue as Cann et al.'s paper, and it was recognized widely in the scientific debate, as suggested by repeated references to "Eve theory" or "Eve hypothesis" in the heated exchange in *American Anthropologist*. A January 1988 *Newsweek* feature, titled "The Search for Adam and Eve," was instrumental in turning Eve into a popular figure (Tierney 1988). The issue's cover depicts a dark-skinned couple in a garden: the woman holds an apple, the man places his empty hand under it, and there is a tree and a serpent in the background. Although culturally provocative especially in the United States, this mock religious framing did not emerge only from popular sources but was recognized by scientists from the start. For example, Robert Eckhardt's response to Cann and colleagues' paper in an April 1987 issue of *Nature* is titled "Evolution East of Eden" (1987), and the biblical framework persistently appears in the *American Anthropologist* debate, as when the multiregionalists portray Eve as "the equivalent of the Garden of Eden and the embarkation point for Noah's Ark rolled into one" (Frayer et al. 1993, 33), and their opponents quip that "the Bible does not identify exactly where Eve lived!" (Stringer and Bräuer 1994, 421). The scientific and cultural debates about Eve, then, were mutually entangled.

My focus here is neither on the biblical imagery that the Eve debate invoked nor on the cultural tensions between mitochondrial ancestry and the biblical narrative of creation—both phenomena that US journalists writing in the context of the evolution-creation controversy sometimes endorsed. Instead, I focus on the cultural emotions pertaining to race, gender, and sexuality that Mitochondrial Eve invoked, since the forms of belonging arising through today's population genetic practices are closely connected to the changing meanings assigned to these categories of difference. The opening paragraph of the *Newsweek* article indicates that Mitochondrial Eve was seen as potentially challenging gendered and racialized categories. The text imagines the mitochondrial ancestor as the polar opposite of "the weak-willed figure in Genesis, the milk-skinned beauty in Renaissance art, the voluptuary gardener in 'Paradise Lost'"

(Tierney 1988). This new Eve is a "dark-haired, black-skinned woman, roaming a hot savanna in search of food," who is "as muscular as Martina Navratilova, maybe stronger" and "might have torn animals apart with her hands" (Tierney 1988). The text also insists that this Eve was not "necessarily the most attractive or maternal" woman living at the time, thereby refusing to define her through culturally sanctioned femininity, maternal attachment, or heterosexual romance (Tierney 1988).

The proto-feminist heroine of the *Newsweek* article also participates in cultural and scientific debates about racial difference. She is "black-skinned" and "dark-haired" and yet the "10,000th-great-grandmother" of every human being of any racial background, thus embodying the instability of racial categories in contemporary society (Tierney 1988). At the same time, her figure encapsulates many population geneticists' attempts to distance their field from assumptions of genetically coded racial differences while insisting that genetic differences between populations help shed light on the secrets of human evolution.[5] A quote from paleontologist Stephen Jay Gould in the *Newsweek* article explicates this position. Echoing the celebratory tone that underlies much of the text, Gould sees mitochondrial analysis as "tremendously important" because it points to a "biological brotherhood that's much more profound than we ever realized" (Tierney 1988). The molecular differences in mitochondrial inheritance between human populations, then, are seen as evidence of the underlying unity of the human species.

The embodied image of Mitochondrial Eve that emerges in the *Newsweek* article is ambiguous in several ways. As suggested above, it erases the original statistical framing of Cann, Stoneking, and Wilson's 1987 article. Yet the very idea of Mitochondrial Eve relies on mathematical calculations and computer models that are in the heart of population genetics. Furthermore, Gould's reference to "brotherhood" contradicts the premise that mitochondrial genealogy is strictly maternal. This idea of brotherhood finds support in the rhetoric of "family trees," "a family record," and "one great family" evoked throughout the text (Tierney 1988). Such familial language is not new in evolutionary theory: Darwin himself deployed familial metaphors to describe the relationships between species in the natural world (e.g. Beer [1983] 2000). In the context of matrilineal inheritance and the proto-feminist image of Mitochondrial

Eve, however, familial language risks trivializing gender by highlighting the family as a kind of natural, nongendered organism that extends in different temporal and geographical directions. The idea of an evolutionary brotherhood then regenders the familial entity, aligning it with symbolically male genealogy. For example, Eve opponent paleoanthropologist Milford Wolpoff is quoted as suggesting that if Eve's descendants replaced all other lineages, "maybe the theory should be named after her murderous son, Cain" (Tierney 1988). This regendering of origins also underlies the article's invocation of scientists' pioneering attempts to identify a genetic Adam. The text's conclusion highlights this message by suggesting that Eve's father could be seen as the Adam of all humans. Such ambivalence between female autonomy and male primacy indicates that the figure of Mitochondrial Eve resonated with mutually contradictory cultural narratives of gender.

All in all, the proto-feminist and dark-skinned Eve that emerged in the *Newsweek* article was a highly affective figure. This affective potential arose partly from the status of *Newsweek* as one of the biggest weekly news magazines published in the United States and known for taking up widely interesting and potentially controversial contemporary phenomena. At the same time, the interpretative ambivalence described above was central to the affective appeal of the "Eve theory." While the idea of a uniform human evolutionary community promoted in the article played with issues of multiculturalism in American society, the feminist undertones of Eve's portrayal touched on societal debates about gender equality and female sexual autonomy. Both affective investments played a central role as other media took on Eve's story.

Eve's Fall

The ensuing coverage of Mitochondrial Eve in the English-speaking media introduced further variations of gendered imagery. A key shift involves the portrayal of Eve as a fashionable but unsubstantiated idea and thus as a purely imaginary figure. For example, in a text published in the popular science magazine *New Scientist*, Wolpoff, Alan Thorne, and Roger Lawn continue their scientific critique by characterizing Eve as "a

newspaper celebrity" and "the brainchild of Allan Wilson" while asking: "Did Eve really exist, or is she an illusion?" (Wolpoff et al. 1991). Similarly, a 1992 *Newsweek* article that drew on the criticism of the mitochondrial theory was titled "Eve Takes Another Fall" (Begley 1992). The article describes Mitochondrial Eve as "a sensation," refers to Wilson's team as "Eve's creators," and insists that "now Eve has gone the way of all flesh" (Begley 1992). Instead of the prehistoric hunter with the strength of a female tennis champion, we encounter here a fragile figure associated with the fickleness of popular stardom and, by implication, idealized femininity. Furthermore, she is portrayed as others' creation rather than her own autonomous self.

This invocation of celebrity culture is reinforced through the discourse of fame and glory. For example, the *New York Times* refers to the "glorious moments" of Eve's discovery by Wilson and colleagues, while insisting that "[t]he glory was short lived" (Angier 1990). Celebrity culture and scientific culture appear here as parallel phenomena, in which overambition leads to an inevitable failure. This end is given religious and moral significance through the rhetoric of the biblical fall, invoked, for example, in the description of "Eve's expulsion from the African Garden of Eden" in the British newspaper *The Independent* (Kohn 1993). As a product of scientists' blind ambition, Eve embodies her biblical namesake's assumed shortcomings such as impatience, unreliability, and weak-willedness.

Apart from being a fickle and material gal, Eve also loses her autonomous and potentially ambiguous sexuality suggested by the muscular and self-sufficient figure of the 1988 *Newsweek* article. This takes place through references to Eve's biblical counterpart, Adam. For example, while imagining Eve as "the single putative matriarch," the *New York Times* emphasizes that "she obviously needed the help of a male to pass her mitochondrial genes along" (Angier 1991). While an egg and a sperm are needed to produce human offspring, the language of naturalness ("obviously") plays with cultural expectations about heteronormative gender roles, such as strong men supporting weak women ("the help of a male"). Similarly, the 1992 *Newsweek* piece begins with the words: "They called her Eve. She was born not of Adam's rib but out of a marriage of silicon and DNA" (Begley 1992). Such a framing associates Eve theo-

rists'—and, by implication, Eve's—assumed failure with Eve's transgression against the logic of female subordination to male sexuality. This suggestion is echoed in an article published in *The Times* in the United Kingdom, which reports that a group of scientists claim that "[d]escent from a single Eve-like figure would leave us bereft of the protection of our complex immune system: the effects of AIDS show how unlikely our species' survival would have been under such conditions" (Hammond 1994). This portrayal renders Eve antithetical to continuity, replacing her with the multitude of reproducing heterosexual ancestors. By invoking the AIDS epidemic, it also associates Eve with the threat of contagion and presumably uncontrollable sexuality.

There is a curious imbalance between the treatment of gender and race in the news coverage of Mitochondrial Eve. While Eve's gender and sexuality are repeatedly reimagined throughout the 1990s, they remain integral parts of her story. This is not the case with race. Compared to the explicitly visualized dark-skinned woman in the 1988 *Newsweek* feature, the Eve invoked in the media in the following years is oddly nonracialized. Although often referred to as "African Eve," the emphasis falls on her being an Eve rather than an African. Similarly, while the widely repeated invocation of "a mother of us all" (e.g. Angier 1991) implies that we are all ultimately African, it distinguishes this imagined, idealized prehistoric cradle from the postcolonial realities of the African continent, as science studies scholar Kim TallBear has observed (TallBear 2013, 519).

The fantasized prehistoric "Africa" thus emerges as a conveniently blurry object with a range of possible connotations depending on the context in which Eve's story is told. The way the story of Eve's Africanness traveled across the English-speaking global north suggests that the idea of a symbolic return to an African "home" carried wide cultural appeal. Yet it engaged in different kinds of affective work in different national contexts. The idea of African origins had particular resonance in the United States, where a considerable part of the population has descended from enslaved Africans. Within the United States, the idea of an African home of all humanity was able to invoke a sense of historical reconciliation, on the one hand, and a sense of threat to the perceived Anglo-Saxon roots of the nation, on the other.[6] In the United Kingdom, debates about multiculturalism are deeply anchored in the history of

the British Empire. Thus the idea of shared African origins resonates with a sense of shame over the injustices of the British rule, while also alarming those engaged in nostalgic regret over the fall of the empire after World War II.[7]

The persistence of gendered and racialized imagery in the news coverage shows that anxiety about gender, race, and sexuality underlay the idea of mitochondrial ancestry from the very beginning. All in all, the shift from *Newsweek*'s initial strong-willed and dark-skinned Eve to a fickle and symbolically white "mother of us all" points to foundational ambivalence in the emotional investments of mitochondrial ancestry. It also reveals considerable flexibility in how cultural emotions about gender, sexuality, and race may be appropriated: while the autonomous African ancestor celebrated female initiative, the fickle feminine figure placated a cultural sense of unrest raised by the former's subversion of proper gender and racial relations. As we shall see next, the affective underpinnings of gender, race, and sexuality became increasingly pronounced with the introduction of Y-chromosome Adam in 1995. At the same time, the idea of Eve as a mere statistical estimate was buried under gendered and racialized cultural narratives.

The Original Couple

As we saw above, the *Newsweek* feature from 1988 already invoked the idea of a genetic Adam, Eve's prehistoric counterpart. In November 1995, the journal *Nature* published two papers on Y-chromosome ancestry. Both studies were based on the observation that while other chromosomes come in pairs, the Y-chromosome is not paired with another Y-chromosome in human reproduction. This meant that the Y-chromosome included nonrecombining genetic material, which could be used as a molecular clock similar to mtDNA. Michael F. Hammer from the University of Arizona reported on having examined 16 human and 4 chimpanzee Y-chromosomes (Hammer 1995). His analysis suggested that the common ancestral human Y-chromosome, to which all current Y-chromosomes can be traced, appeared approximately 188,000 years ago. Hammer found "no evidence for a recent, strong

selective sweep on the human Y chromosome," emphasizing a steady process of molecular evolution (Hammer 1995, 376). Hammer's article was followed by a paper by Simon Whitfield, John Sulston, and Peter Goodfellow from Cambridge. Based on their examination of five human and one chimpanzee Y-chromosomes, Whitfield and colleagues estimated that the ancestral human Y-chromosome was only 37,000–49,000 years old (Whitfield et al. 1995). They speculated on a recent "selected sweep of an advantageous Y chromosome or extensive migration of human males," highlighting the possibility that the surviving Y-chromosome may be connected to—possibly even contributing to—a particular pattern of male behavior (Whitfield et al. 1995, 379). This invocation of prehistoric gender roles and reproductive strategies echoed the claims made in the field of evolutionary psychology, which arose in the early 1990s to study human behavior and cognition as products of evolution.[8]

While the *Nature* articles used the language of statistical estimates and ancestral Y-chromosomes, the media framed the news as concerning a real, embodied male ancestor, who provided a counterpart for Eve. For example, the *New York Times* explained that "scientists think they have found strong evidence that there was an ancestral 'Adam' about 188,000 years ago to go with the previously discovered 'Eve'" (Wilford 1995). This framing was emphasized in accounts with a less matter-of-fact tone, as when a commentary published in the British paper *The Independent* refers to "Mitochondrial Eve and her friend African Adam," describing the former as "the girl they dug up a few years ago" and the latter as "the equivalent chap" (Hartston 1995). Such playful language extends the popular imagery associated with Eve the fickle celebrity to the figure of Adam, a prehistoric "chap" and Eve's "friend." While this rhetoric is consistent with the genre of news commentary, it also points to the ease with which a scientific report can be embedded within a culturally familiar narrative framework.[9]

The narrative invoked in the press coverage was explicitly heteronormative. The above-quoted *New York Times* article illustrates this point. After noting that Michael Hammer had located the common ancestral Y-chromosome "reasonably close to the time for the common mitochondrial ancestor," the text continues: "Mitochondrial Eve, meet

Y-chromosome Adam" (Wilford 1995). While the text reports that Mitochondrial Eve and Y-chromosome Adam "could have lived at slightly different times" and that they "were probably two random individuals in the small population of early humans," it nevertheless quotes Hammer's "joking" response to the possibility that Adam and Eve lived on different continents: "It would just mean that Adam and Eve must have run up some big phone bills" (Wilford 1995). The fact that the quote is from Hammer himself suggests that scientists played a key role in the erasure of the language of statistical estimates and the emergence of Eve and Adam as embodied historical figures. That journalists highlight such familiar heteronormative narratives in turn reinforces cultural assumptions about what kind of knowledge science can—and should—offer contemporary societies. As a result, such playful statements as "The genetic Eve gets a genetic Adam" and "Now, Eve has an Adam" (U.S. News & World Report 1995) root popular ideas of heterosexual courtship in an imagined prehistoric landscape, while shoring up the role of genetics as the privileged gateway to human relationships.

This heterosexual courtship plot invokes cultural ideas of masculinity and femininity. For example, the description of the Y-chromosome as "what makes a man a man" (Milius 1995) operates in a circular fashion, invoking an unspecified set of assumptions about how men are different from women. Likewise, the portrayal of the Y-chromosome ancestor as "the original dad" invites common assumptions about family dynamics, including ideas about patriarchal heads of the family (Milius 1995). This potential to cater to the popular imagination becomes evident in a 1998 *New Scientist* article titled "All about Adam." The text describes the Y-chromosome as "a guy thing" and declares that "[w]ags [wives and girlfriends] will tell you it's the site of the genes for incessantly clicking the TV remote control and for the excruciating embarrassment that accompanies asking a stranger for directions" (Jensen 1998). The text then states that "a small band of pioneering researchers is now finding that the Y chromosome is an unmatched repository of human evolutionary and behavioural information," and that "[w]armongering and polygamy have both played their part in determining human genetic inheritance. Only Y chromosome analysis will reveal the evolutionary significance of history's Genghis Khans and Casanovas" (Jensen 1998). Here, genetic ances-

try is given an evolutionary psychological interpretation that posits a genetically controlled desire to propagate as the driving force of human behavior, a representation that echoes Whitfield et al.'s (1995) *Nature* article. Headlines like "Adam and Eve's children" in the Montreal paper *The Gazette* reinforce this reproductive framing (Wade 2000). Tellingly, the piece in question did not actually claim that Adam and Eve reproduced together, but simply discussed the range of haplogroups (inherited combinations of genetic markers) that the ancestral Y-chromosome and mtDNA gave rise to.

The heterosexual courtship plot was given another twist in November 2000, when Peter Underhill at Stanford University and a number of colleagues published a paper that estimated that the human ancestral Y-chromosome emerged as recently as 35,000–89,000 years ago (Underhill et al. 2000). The newspaper headlines invoked the familiar courtship framework: *The Daily Telegraph* in London promised to tell "How Eve Was Left Waiting for Adam" (Derbyshire 2000), the Melbourne *Herald Sun* stated that "Adam Had No Eve" (Williams 2000), and the Canadian *Calgary Herald* declared: "Adam, Eve No Couple" (*Calgary Herald* 2000). These similarities attest to the ways in which the conventions of science journalism travel globally (O'Mahony and Schäfer 2005), as well as to the resonance of the courtship plot across English-speaking culture.

One prominent version of the heterosexual plot was the narrative of the battle of the sexes. Totally misunderstanding the science, the Scottish *Daily Record* announced that "Men Are 84,000 Years Behind Women; DNA Proves Gap" (*Daily Record* 2000), and the Melbourne *Herald Sun* suggested that "[f]emale genes were early developers" (Williams 2000). In a similar vein, the Plymouth, UK, paper *Western Morning News* answered the question "What Eve Was Doing Before She Met Adam" with the tongue-in-cheek speculation that Eve "was breeding … with a male less developed than she or, depending on your viewpoint, the male has now evolved one stage further while womankind has remained its primitive original self" (*Western Morning News* 2000). One particularly skillful appropriation of cultural vocabulary appeared in *The Scotsman*. The piece suggested that "Adam may have had a soft spot for the Garden of Eden's apples, but he must also have found it impossible to resist older

women, it emerged yesterday. … So based on the findings of researchers at Stanford University in California, Adam was not only the first man, he was undoubtedly a toy boy of biblical proportions" (Montgomery 2000). These variations of the courtship plot point to its flexibility as a cultural narrative. They also suggest that it carries considerable affective potential through which ideological commitments concerning gender, sexuality, and knowledge can be evoked and reinforced. Humor plays a crucial role in this affective dynamic, as it persuades us to acknowledge as natural the gendered order that such appropriations of the courtship plot rely on.

We saw above how the language of "mother of us all" renders the imagined prehistoric Africa symbolically white. The discourse of heterosexual courtship reinforces this representation of race. The portrayal of Adam and Eve as our shared original parents invokes a temporal dynamic that posits Africa as a realm of the past. The 1998 *New Scientist* article quoted above explains that scientists found "the ancestral haplotype—nuclear Adam—by looking at the corresponding section of Y in chimpanzees, gorillas and orang-utans," which turned out to match "the one Underhill found in small human populations in northern and southern Africa" (Jensen 1998). This portrayal continues the old colonial representation of Africa as belonging to an earlier, not-quite-human evolutionary stage. As Kim TallBear (2013, 519–520) demonstrates, this kind of rhetoric denies contemporary Africans access to modernity, leaving them outside the collective "us" whose history scientists and science journalists are narrating. This does not mean that differences between contemporary populations would not count—quite the contrary, the geographic diversity of molecular material is the precondition of mitochondrial and Y-chromosome analyses. However, differences between populations are subjugated to the symbolically white cultural framework through which the mitochondrial and Y-chromosomal ancestors are made sense of.

The fantasized reproductive coupling of Adam and Eve adds to this rhetorical dynamic. The language of dating, phone bills, and toy boys posits western culture as the primary frame of interpretation for scientific innovation, while the courtship plot itself reflects a familiar western way of organizing emotions and expectations. Associated with a symbolically reproductive mission, Adam and Eve cease to be geographically located individuals (the initial popular view) or random carriers of particular

genetic structures (the scientific view), and come to stand for what is imagined as the fundamental, biological heterosexual dynamic. In her discussion of genetic imagery in the 2004 Summer Olympic Games opening ceremony, Catherine Nash suggests that the valorization of a single, symbolically reproductive couple in the public spectacle echoed a "contemporary vocabulary of universal humanity" while positioning the couple as "that which transcends cultural difference" (Nash 2005, 450). This observation also applies to the public life of our imagined prehistoric couple. Through their fantasized reproductive union, Mitochondrial Eve and Y-Chromosome Adam promise reproductive continuity, while substituting universal human experience for racial differences. As with the Olympic couple, this universality is of course illusionary.[10]

Eve and Adam as Affective Objects

These shifts in the cultural reception of mitochondrial and Y-chromosome analyses and the figures of Mitochondrial Eve and Y-Chromosome Adam are above all an account of travel: the travel of gendered narratives, racialized imageries and assumptions about knowledge across textual genres and cultural contexts. Such travels suggest that popular narratives about science undergo transformations that open up new interpretations. In so doing, they also give rise to multiple forms of genetic belonging—an issue that I address in the following chapters. The role of race is a prime example of this affective, narrative, and ontological malleability: while the introduction of the idea of a global human family generated considerable appeal across the global north, it was enacted differently, say, in the context of African American history or British multiculturalism. The cultural travels of Mitochondrial Eve also demonstrate the ease with which the language of statistics and computer models is replaced by the language of fleshed embodiment and identity discourse.

This imaginative flexibility is part of Eve and Adam's appeal, as it enables the invocation of a range of cultural emotions. Such emotions invite the audiences to sympathize with particular ideological positions, thus engaging in cultural negotiations over what kinds of futures contemporary science should strive for.[11] Feminist and postcolonial scholar Sara

Ahmed's work on affect provides an interesting viewpoint into these emotional engagements. What makes Ahmed's approach particularly useful for my discussion of mitochondrial and Y-chromosome ancestry is her focus on the ways in which objects—in this case, mtDNA and the figure of Eve—become invested with emotions. Unlike many affect studies scholars, Ahmed does not distinguish between emotions and affect, but understands them as part of a cultural dynamic in which embodied sensations, nameable emotions and social structures are entangled.[12] In *The Cultural Politics of Emotion* (2004), Ahmed argues that emotions should not be understood as things we "have" but as orientations through which we "respond to objects and others" (Ahmed 2004, 10). For Ahmed, "[e]motions are both about objects, which they hence shape, and are also shaped by contact with objects" (Ahmed 2004, 7). Ahmed connects this dynamic to an underlying capitalist logic. In such a logic, "affect does not reside positively in the sign or commodity, but is produced as an effect of its circulation" through a web of shifting associations (Ahmed 2004, 45). Hence, "the more signs circulate, the more affective they become" (Ahmed 2004, 45).

This process of circulation results in objects becoming "sticky, or saturated with affect, as sites of personal and social tension" (Ahmed 2004, 11). Such stickiness is not, however, equally distributed. Some figures and bodies—those of racial and sexual minorities for example—are more likely to emerge as affective objects toward which and through which emotions take shape. The circulation of objects is also characterized by what Ahmed calls "metonymic slide" (Ahmed 2004, 44). Certain objects become mutually associated with the result that the evocation of one effects the invocation of another. According to Ahmed, this "sideways movement between objects … works to stick objects together," so that emotions emerge and travel through chains of movement and displacement (Ahmed 2004, 66). Crucially, this logic of circulation makes emotions both persistent and malleable: they can be directed toward new phenomena while adhering to old objects and positions.

The debate about Mitochondrial Eve is characterized by a series of metonymic slides. As Cann and colleagues' mitochondrial theory of recent African origins moved from the lab to the journals to the media, the object of the debate metamorphosed from a molecular estimate to a

hypothetical historical person to a culturally provocative female figure to a fantasized heterosexual union. At one end of this spectrum, we have Allan Wilson's laboratory in California, where scientists are collecting and analyzing human tissue and trying out different statistical methods to produce a web of genetic difference and distance. Such a web is, by its very nature, always theoretical, so that changes in laboratory practice produce new sets of connections, as we saw in the case of the different estimates of Y-chromosome ancestry by Hammer (1995), Whitfield et al. (1995), and Underhill et al. (2000). Furthermore, as Amade M'charek observes, mtDNA as a scientific object is fundamentally fluid: Cann and colleagues' mitochondrial paper relied on constructed entities such as the 1981 Cambridge reference genome for human mitochondria, or the rapidly mutating HeLa cells (M'charek 2005, 84–119). At the other end of the spectrum, we have emotionally appealing appropriations of mitochondrial theory, such as geneticist Bryan Sykes's popular science book *The Seven Daughters of Eve*. Published in 2001, Sykes's book explores the maternal lineages that connect modern Europeans to seven hypothesized female ancestors, from whom the mitochondrial haplogroups present in European populations allegedly stem. Through its familial language, Sykes's book imagines an emotionally loaded bond between Mitochondrial Eve, her seven symbolic "daughters," and modern Europeans. A number of metonymic slides have taken place between the two endpoints of the spectrum, "sticking" molecular entities to gendered and racialized cultural figures—the shared mother, the attention-hungry celebrity, Adam's girlfriend—in ways that cannot be easily undone. Through this process, feelings of surprise, anxiety, longing, and belonging have been evoked, rejected, and reinforced.

This affective multiplicity shapes the ways in which gender, sexuality, and race intersect in the mitochondrial debate. For example, Africanness is located in a prehistoric scene preceding the universalized couple and their fantasized progeny through a series of associations, which connect a continent, a matrilineal form of ancestry, premarital and extramarital sexuality, and not-quite-human bodies into an undefined and resonant cultural entity. In the process, race is sexualized, sexuality is racialized, and gender is heterosexualized in ever new ways. As with molecular objects, slight shifts in how intersecting differences are imagined may

change the emotional commitments of the story. Priscilla Wald (2000) offers an intriguing reading of such narrative revisions in the media coverage of a possible genetic link between susceptibility to HIV among African Americans and the geographic spread of the bubonic plague in medieval Europe. Wald argues that both the science behind the news and the journalists' accounts of it understood genetics as "a genealogical system that maps not just relationships but rules that govern relatedness" (Wald 2000, 705). These patterns of genetic inheritance were imagined by some journalists in pseudo-evolutionary terms as indicating black weakness and white survival (Wald 2000, 705).[13] Wald observes that this logic of genetic kinship replaced the politics of affiliation central to HIV activism with heteronormative language of white familialism, thus dismissing the affective resources of queer communities and communities of color. In other words, such an imagined "genetic diaspora incorporates white men and women, regardless of their choice of affiliation, on the basis of their genes," thereby engendering "a community that one cannot not join: an inalienable community" (Wald 2000, 694). At the same time, the imagined genetic diaspora leaves other racialized or ethnic identities and other sexual practices outside the logic of ancestry.

The mitochondrial debate, too, is underwritten by a similar reconfiguration of the affective potential of genetic kinship. The differences between the 1988 and 1992 *Newsweek* articles discussed above demonstrate the point: while the former text posits the intersection of visibly nonwhite origins and fantasized female strength as a cause of celebration, the latter constructs the same intersection as a source of misguided belief. In the heart of this discursive shift is the idea of reproduction. Whereas the first *Newsweek* article envisions reproduction as universal connectedness that ties together the whole human species, the second text equates genetic ancestry with symbolically western heterosexuality. In so doing, both accounts tap into popular vocabularies invested with cultural resonance and affective potential. At the same time, they clearly depart from the understanding of genetic kinship as statistical correlation and shared molecular characteristics in Cann, Stoneking, and Wilson's 1987 paper or the subsequent population genetic literature.

The Threat of Maternal Rebellion

The recurring portrayal of Eve as representing false science as well as wrong kind of femininity indicates that her figure invoked anxieties over the idea of maternally defined history. I want to take a closer look at this affective investment, as it elucidates how mitochondrial and Y-chromosome technologies are entangled with cultural politics of gender and sexuality. To this end, I turn to a popular horror novel that builds on the debate surrounding Mitochondrial Eve. Hideaki Sena's *Parasite Eve* was published in Japan in 1995 in the midst of the mitochondrial debate, and translated into English and published in the United States in 2005. Premised on the maternal inheritance of mtDNA, the novel tells the story of "Eve," a self-conscious mitochondrial life-form that seeks to take over the world by controlling people's bodies and minds through their mitochondria. The novel focuses on a male scientist, Toshiaki Nagashima, whose wife Kiyoshi is in coma after a fatal car accident. The accident was orchestrated by Eve, who has lived in Kiyoshi's cells and manipulated her behavior and emotions. After Kiyoshi is declared brain-dead, one of her kidneys is transplanted into a young woman, Mariko, who becomes the inadvertent host of the dangerous and destructive mitochondrial enemy. Eve also manipulates Toshiaki to take a tissue sample from Kiyoshi's liver and to use it to grow an immortal cell line, "Eve 1." The novel culminates in Eve's plan to use Toshiaki's sperm and Mariko's womb to give birth to a powerful mitochondrial "daughter" that will rule the world, ending with Toshiaki's and Mariko's father's attempts to stop Eve and her "daughter."

The novel makes it clear that the threat that Eve poses to humanity is a specifically feminine threat. Eve muses about her own existence and purpose:

> She had endured countless millennia, dreaming this day would come. She had endured the meek role of producing energy as Her host commanded. She would always do so as long as She was provided sustenance, Her host simply never doubted Her submission, happily unaware that instilling this very arrogance had been part of her plan. (Sena 2008, 205–206)

The use of capitalized feminine pronouns suggests that Eve represents ultimate femaleness. She is a treacherous plotter, who has merely pretended to accept the role of subservience often ascribed to conventional femininity. In fact, however, "She was the mistress, nuclei Her servants," as her true plan is "to create a daughter of Her own will, a life form even more perfect than She. An Eve for the new world" (Sena 2008, 208). Eve's essential femaleness is also suggested by the way in which Toshiaki's student Asakura, who takes care of the mitochondrial culture grown from Kiyoshi's cells, senses that she "understood Eve 1 not by observation, but by intuition," that quintessential feminine characteristic (Sena 2008, 129). Eve's gender is also underlined by the explicitly sexual quality of her attention to Toshiaki, whom she sees as the only man "who would truly understand Her, finally appreciate Her" (Sena 2008, 206). Through her control over Kiyomi's cells while Kiyomi is still alive, Eve is able to savor and indulge in Kiyomi and Toshiaki's lovemaking, thinking that "it wasn't Kiyomi that Toshiaki was making love to. **He was making love to ME**. The ecstasy that rippled through Her entire being now was nearly enough to make Her swoon" (Sena 2008, 206; emphasis original). The idea of exclusively female revolution thus becomes connected to a heterosexual dynamic that, through Eve's forced seizure of Toshiaki's sperm later in the novel, takes the shape of the familiar narrative of the battle of the sexes.

In *Parasite Eve*, sexuality serves ultimately reproductive purpose: the creation of Eve's powerful daughter through the conjoiner of Toshiaki's sperm and Eve's cultivated cell line. Reproduction, in turn, is tied to the parallel histories of mitochondrial and human evolution, in which reproduction is seen as a means to futurity. Toward the end of the novel, Eve invades Asakura's body and announces herself through the conference presentation Asakura is giving: "Until now, I have spent most of my life living inside your bodies. I have seen all of your history that has come to pass and retain it in my memory" (Sena 2008, 216). Rather than seeing mitochondrial evolution as part of human evolution, Eve posits the two as antithetical to one another. Furthermore, the parallel histories of mitochondrial and human evolution are tied explicitly to the debate concerning Mitochondrial Eve. "Mitochondrial Eve did indeed exist in Africa," Asakura's parasite declares: "I can even tell you exactly where. Why, you ask? Because I retain the memory. I was Mitochondrial Eve. Of course,

even before then, I was lurking in that life form you call 'Lucy'" (Sena 2008, 217). The novel's "parasite Eve" thus appears as ruling over the discoveries of not only population genetics (embodied in the figure of Mitochondrial Eve) but also paleontology (embodied in the famous *Australopithecus afarensis* fossil Lucy). Crucially, the parallel histories of human and mitochondrial histories that are made visible through Eve's declaration are not presented as equal. Eve sees humans as essentially inferior, as they fail to reproduce as fast as mitochondria: "I change ten times faster than your genomes. This means that I evolve ten times faster than you. The history of your evolution has always been a victory of my making" (Sena 2008, 218). Hence, she informs her audience, "[t]he prosperity of the world will be in the hands of my descendants … Unfortunately, none of you will be around to witness this miracle, for you *Homo sapiens* will be annihilated" (Sena 2008, 218–219).

This portrayal of mitochondrial inheritance as a specifically female lifeform that threatens to quash the human species through its parasitic existence feeds from the sense of anxiety and discomfort that the proto-feminist figure of Mitochondrial Eve raised. In particular, the novel's emphasis on the rapidity of mitochondrial evolution registers hopes and anxieties surrounding the key role of reproduction in evolutionary narratives of survival and extinction.[14] Such hopes and anxieties are not, however, exclusive to public or popular discourse. Although the events of Sena's novel are fictional, its affective politics find support in the science that inspired it. An interesting point of reference is the widespread use of the HeLa cell line in science laboratories around the world. The HeLa cells were collected in the early 1950s from an African American patient, Henrietta Lacks, who died of an unusually aggressive cervical cancer at Johns Hopkins University Hospital in Baltimore. Lacks's cancer cells turned out to be dividing so rapidly that they were used—without Lacks's or her family's consent—to produce the first immortal cell line. Such a cell line could be cultured, transported, and used seemingly endlessly in scientific experiments across the world. Indeed, the HeLa cell line provided one source of mitochondrial information in Cann, Stoneking, and Wilson's 1987 mitochondrial paper. Intriguingly, scientist and science studies scholar Lisa Weasel (2004) demonstrates that mediated emotions and cultural images organize the use of HeLa cells in laboratories. Weasel

documents how the unusually aggressive growth of HeLa cells became widely associated with promiscuous female sexuality, which in turn was linked to women of color through the figure of Henrietta Lacks. This engendered the view that through their inherent promiscuity HeLa cells contaminated all cell cultures that they came into contact with, threatening the purity of samples, the ordered world of the laboratory, as well as the practices of circulation that gave scientists access to samples necessary to guarantee the progress of science. Sena's description of Kiyomi's cells in *Paradise Eve* resembles closely the story of HeLa cells. Like the famous HeLa cells, Kiyomi's cells "were dividing at a rate faster than common cancer cells" (Sena 2008, 125). They react wildly to chemicals introduced to the culture, extruding from any dish that tries to contain them. Read together, then, the history of the HeLa cell line and Sena's fictional account of power-hungry mitochondria suggest that assumptions about molecular matter take shape through a cultural politics of emotion, turning a cell line or a molecular entity into an affective object through which anxieties and prejudices about gender, race, and sexuality are articulated and reshaped.

The genre conventions of the horror novel operate as a crucial mechanism through which this affective dynamic is produced in Sena's text. The novel's plot is highly formulaic, as Eve's treacherous operations are pitted against central characters' attempts to save Mariko and outwit Eve. In this respect, the novel resembles the "outbreak narratives," accounts of the emergence and spread of a deadly virus, that Priscilla Wald (2008) has traced in popular fiction and film. In outbreak narratives, a new powerful virus or other microbe poses a threat to the whole humanity as well as the gendered orders of national communities, while heroic scientists try desperately to find a way of containing or undoing the pathological agent's destructive aspirations. In such a scenario, the disembodied rationality of science is the ultimate antidote to the menacing, boundary-breaking materiality that the virus—or in Sena's novel, mitochondria—embodies. This posits the power to manipulate affective responses as internal to the molecular enemy rather than the presumably rational science. At the same time, the affective power of the narrative itself relies on the emotional responses that such representational politics engenders in the readers. In Sena's novel as well as the narratives analyzed by Wald, this effect

is sought through explicit descriptions of the violence engendered by the enemy: bursting tissues, burning bodies, gushing bodily fluids. In such descriptions, affective work becomes intimately connected with bodily materiality.

The threat posed by the maternal lineages of mitochondrial inheritance, then, appears as an explicitly material threat. It is materiality that overflows the proper boundaries of gendered social order.[15] In *Parasite Eve*, mitochondria make women act in nontraditional ways, as when Kiyomi throws herself into lustful sex with Toshiaki or makes bold statements while attending an academic presentation, or when Asakura, possessed by Eve 1, bossily dismisses her audience at a conference. Crucially, this suggests an alternative politics of materiality to the one seen in the media reception of the theory of Mitochondrial Eve. While the debate surrounding Mitochondrial Eve in the media turned an abstract, statistical inference into a culturally recognized female figure, Sena's novel portrays mitochondrial materiality as a mass of melting and mutating flesh that changes from a perfect imitation of the beautiful and feminine Kiyomi to a giant, all-consuming vagina whose only purpose is to seize Toshiaki's sperm. Such politics of gendered materiality indicates that the embodied figure of Mitochondrial Eve that Cann, Stoneking, and Wilson's paper introduced, and the ensuing public debate gave meaning to, resonated with long-standing anxieties about wild, reckless, and unpredictable female nature.

From Global Unity to Tribal Specificity

As both Sena's novel and the media reception of Mitochondrial Eve demonstrate, one underlying theme of the debate about mitochondrial and Y-chromosome techniques concerned female agency and the cultural boundaries of femininity. This concern intersected in popular discourse with another theme—race and genetic differences between populations—which underlay both the initial celebration of Eve' Africanness in *Newsweek* and the subsequent downplaying of it in many media texts. In order to examine the hopes and anxieties surrounding the idea of evolutionary racial difference, I shall turn to another work of fiction, Australian

science fiction writer Greg Egan's short story "Mitochondrial Eve." The story shows that like female agency, the question of racial difference is deeply entangled with wider cultural politics of emotion.

Egan's "Mitochondrial Eve" was first published in 1995 around the time when the debate about Y-Chromosome Adam and the connection between mitochondrial and Y-chromosome history became an object of public debate. The novel is set in the (then) future in the years 2007–2017. The story is told by a first-person narrator, physics postdoctoral researcher Paul, who is persuaded by his new girlfriend Lena to have his mitochondrial inheritance "mitotyped," that is, to have it compared to the mitochondrial haplogroups of world populations. The test is conducted by a company called the Children of Eve, which Lena fervently supports. Lena persuades Paul to apply for money from the Children to develop a new method of mitochondrial analysis based on his knowledge of physics. If completed, this method would enable the Children to produce a comprehensive mitochondrial family tree for the whole humanity. What adds urgency to the project is the newspapers' declaration that scientists have found an ancestral Adam that may displace Eve as everyone's ultimate ancestor. This development leads to the appearance of Adam's supporters known as "Sons of Adam." The question of mitochondrial versus Y-chromosome ancestry soon emerges as a political question embedded in both gendered and racialized ideologies. Toward the end of the novel, what began as a seemingly innocent battle of the sexes becomes increasingly violent "Ancestor Wars" in which assumed differences between not only genders but also racially coded populations are appropriated and reinforced.

The novel reflects the insistence familiar from the media coverage of Mitochondrial Eve that population genetics is able to produce a concrete and precise history that connects us to a specific embodied woman. When Paul has his DNA mitotyped, the results are presented as placing him in an absolute, nonnegotiable web of relatedness, as Paul is shown "the face of one of [his] living 6000th cousins" (Egan 2008, 35). Lena confirms this belief in accuracy: "You are a Child of Eve, Paul. You know who you are, now. And no one can ever take that away from you" (Egan 2008, 32). Crucially, she sees Paul's research project as promising to provide an even higher level of concreteness:

> *This* could transform the whole field. No more guesswork, no more conjecture, no more assumptions—just a single, indisputable family tree, stretching back 200,000 years. … With *quantum paleogenetics*… you'll have the power to bring Eve to life for the world in a way that no one has ever done before. (Egan 2008, 41)

As with the media accounts of Mitochondrial Eve, the hypothetical and statistical nature of Eve and the accompanying web of relatedness is erased here.

Affect plays a crucial role in this production of concreteness. While Paul himself remains skeptical, he recognizes how the Children's campaign evokes affect. When Paul first sees a hologram of Eve at the entrance to the Children's office, he observes that "[t]he artist had rendered our hypothetical ten-thousand-times-great grandmother as a strikingly beautiful woman," a representation that makes him experience "a certain bizarre, involuntary swelling of pride at the sight of her" (Egan 2008, 29). Lena, a true believer in the Children's cause, insists that the Children's message can affect us so powerfully that it may prevent ethnic conflicts: "that deep sense of belonging, through Eve, to a single family which encompasses all of humanity … do you honestly imagine that they could have turned on each other like that?" (Egan 2008, 37). However, affect is a resource that the competing molecular cults—the different clans of Adam—also invoke and appropriate. With the appearance of loud and violent pro-Eve and pro-Adam activists, the affective underpinnings of Egan's narrative change from reaffirmation and celebration to aggression and hatred. The text thus recognizes the inherent multiplicity of the affective engagements of mitochondrial and Y-chromosome technologies that underlay the media coverage of Cann, Stoneking, and Wilson's paper. At the same time, Egan's story imagines and explicates the implications of this affective potential in ways not present in those media texts.

These affective changes result from the blurriness of the levels of analysis that mitochondrial and Y-chromosome technologies enable. This is perhaps the most important point that Egan's short story raises, as it concerns the ways in which mitochondrial and Y-chromosome techniques may be used beyond scientific research to enact multiple forms of

belonging. In Egan's story, the Children's work is based on the assumption that mitotyping should operate on the level of the global, so that people would "acknowledge, explicitly, a common ancestry which transcended their own superficial differences in appearance," and recognize, as Lena puts it, that "[t]his Eve belongs to everyone, equally. Every culture, every religion, every philosophy" (Egan 2008, 30). Such claims are premised on the assumption familiar from the 1988 *Newsweek* article that all people are connected through an underlying, molecular unity. However, the appearance of Adam in Egan's story demonstrates that the global is not the only level on which molecularized belonging may operate. Rather than an ancestor to the whole species, the Adam that the story's journalists announce is a father to particular male populations: the headline "Y-CHROMOSOME ADAM STRIKES BACK!" is accompanied by a picture of "a near-naked, muscular, blond white man (curiously devoid of body hair—rather like Michelangelo's David in a bison-skin loincloth) aiming a spear at the reader with suitable balletic grace" (Egan 2008, 45). In this representation of athletic white masculinity, gender, sexuality, and race emerge as mutually intertwined. In addition to his skin color, physical strength, and suggested sexual appeal, this new Adam represents a specific male lineage that relies on the exclusion of both maternal ancestry and nonwhite ethnicity.

This narrative development also affects how Eve is represented. Encountering the Children's updated rendering of Eve at a genetic ancestry conference, Paul observes:

> The new Eve was slightly paler, her nose a little thinner, her eyes narrower. The changes were subtle, but they were clearly aimed at making her look more 'pan-racial'—more like some far-future common descendant, bearing traces of every modern human population, than a common ancestor who'd lived in one specific place: Africa. (Egan 2008, 47)

While insisting on the idea of universality, this representation attests to the close link between affect and cultural imaginaries. Eve's appeal, the image suggests, relies on her position as Adam's symbolic counterpart, a role enabled by her visual un-Africanization, and tied to a familiar heteronormative dynamic. This detachment of Eve from specific roots also

points to the slipperiness of the concept of universality, as Eve's reconstructed universality necessitates the exclusion of geographically situated, lived specificity. In this respect, Egan's story echoes the representation of the universal couple that emerged in the real-life media coverage of Eve and Adam.

Egan's story emphasizes that the affective tensions between the cults of Eve and Adam result from the level of analysis that scientists and biotechnological companies engage in. These tensions intensify through the accelerating movement away from global prehistory toward the end of the story:

> By 2017, Lena's worst predictions had all come true. Dozens of different Adams had been proclaimed around the world, and the trend was to look for the common paternal lineage of smaller and smaller populations, converging on ever more recent ancestors. Many were now supposedly historical figures; rival Greek and Macedonian groups were fighting it out over who had the right to call themselves the Sons of Alexander the Great. Y-chromosomal ethnic classification had become government policy in three eastern European republics and, allegedly, corporate policy in certain multinationals. (Egan 2008, 51)

Egan's dystopic Ancestor Wars demonstrate how the chosen level of population genetic analysis produces difference, and how this logic of escalating difference is entangled with cultural emotions of primacy and privilege. Through this emphasis on different levels of analysis, the text also captures the blurriness of the concept of population in population genetics. This blurriness, Jenny Reardon (2005) argues, is one of the reasons why the connection between population and race remains unsettled in population genetics, and thus why the relationship between population genetics and racism is fundamentally ambivalent. At the same time, as Amade M'charek (2005, 21–55) observes, the blurriness of population is also a precondition of population genetic analysis. That is, shifts in the level of analysis enable population geneticists to tease out differences among people. I return to the blurriness of the concept of population in Chap. 5 in the context of the idea of population genetic community.

Egan's story also elaborates on the centrality of family metaphors that underlie mitochondrial and Y-chromosome technologies, and that played a central role in the media coverage of Cann, Stoneking, and Wilson's paper. In Egan's story, the work of the Children of Eve is based on familial language. Visitors to the Children's office are welcomed by the sign "ONE WORLD, ONE FAMILY" (Egan 2008, 29), the results the Children provide are referred to as "an ancient network of invisible family connections" (Egan 2008, 35), and each member is called a "cousin" (Egan 2008, 30). Crucially, Eve's opponents employ similar language. Called "the Sons of Adam," the supporters of Adam (or the various more recent tribal Adams) insist on the importance of direct patrilineal inheritance as a basis for belonging (Egan 2008, 48). The acceleration of the story's events toward violence suggests that familial rhetoric is always ambivalent, and potentially politically dangerous, because it relies on a distinction between those who are kin and those who are not. It is important to note that this is not simply a matter of a particular version of family rhetoric, but family rhetoric in general. Despite their focus on universality, the Children of Eve are a party to the exclusionary logic of familialism, as suggested by Paul's comment: "Who made *kinship* such a big issue in the first place? Who did their best to propagate the notion that everything that matters depends on *family ties*?" (Egan 2008, 46). Egan's story thus provides another angle to the exclusions implicit in genetic familialism analyzed by Wald (2000) and Nash (2005) and discussed above. This emphasis on familial lineages has at least two important implications. First, as Nash (2006, 19) observes, by emphasizing direct, intergenerational lineages, mitochondrial and Y-chromosome technologies suggest purity, the untaintedness of inheritance. Second, this kind of "obsession with *pedigree*" (Egan 2008, 30) masks the potential incompatibility of different modes of population genetic analysis or sets of data by engendering a seemingly unified image of descent.

Finally, Egan's short story is particularly poignant when read in the context of current population genetic practices. While the Children of Eve and the Sons of Adam are fiction, there have emerged in the past 15 years a number of online biotechnological companies that promise to trace their prospective customers' genetic ancestry and to define their belonging to the diverging branches of human evolution. Mitochondrial

and Y-chromosome analyses play a key role in these practices. The focus of the tests is precisely on identifying the customers' belonging to ever-smaller genetic groups such as particular mitochondrial or Y-chromosome haplogroups, often framed as "clans." This shows that we have indeed moved from the presumably universal Eve and Adam of the 1990s toward localized clan mothers and clan fathers. Unlike Egan's short story, the real-life testing practices promise to trace customers' relationship not only to many localized Adams but also to multiple localized "daughters" of Eve.[16] This interest in the particular and localized also underlies national genome projects—including the Icelandic and Irish enterprises discusses at the beginning of the chapter—that have emerged since the 1990s. This move from the global to local has changed considerably how we think about roots, borders, and communities, and how those roots, borders, and communities enact specific forms of belonging. These implications are the topic of the rest of the book.

Emerging Trajectories of Belonging

This chapter has explored the emergence of mitochondrial and Y-chromosome analyses within human population genetics, and its entanglement with gendered and racialized politics of affect. As the media reception of Cann, Stoneking, and Wilson's mitochondrial paper and the subsequent studies of Y-Chromosome ancestry by Hammer, Whitfield et al., and Underhill et al. suggest, the figures of Mitochondrial Eve and Y-Chromosome Adam resonated strongly with cultural vocabularies and imaginaries. These included naturalized ideas of heterosexual courtship and the battle of the sexes, as well as competing ideologies of femininity and masculinity. Furthermore, Sena's novel and Egan's short story attest to the affective ambiguity of mitochondrial and Y-chromosome technologies by connecting the debate about Mitochondrial Eve to questions of social threat, societal control, gendered and racialized hierarchies, and the potential collapse of human societies. All in all, the cultural discourses surrounding Mitochondrial Eve suggest that new biotechnological practices may engender moments of openness, moments of possible revision of cultural vocabularies. The debate also indicates that those moments

tend to close quickly, transforming into familiar cultural patterns of gendered and racialized social order.

The chapter has also shown how gender, sexuality, and race intersect in mitochondrial and Y-chromosome technologies and the affective landscape they are entangled with. For example, the media coverage of the mitochondrial debate demonstrates a move from ideas of nonconforming gender, autonomous female sexuality, and original "Africanness" in the 1988 *Newsweek* article to white, yet presumably universal femininity and masculinity. Race, gender, and sexuality are also entangled in the processes through which molecular objects (placentas, DNA samples, the sequenced mitochondrial genome) engender hypothetical constructs (a prehistoric point of convergence inferred through statistical analysis and computer modeling) and, further, embodied figures (strong hunter, fallen woman, superficial movie star). Likewise, gender and race intersect in crucial ways in Egan's representation of the "battle of the sexes" between the Children of Eve and the Sons of Adam as a mechanism of accelerating racial rivalry.

I want to conclude by thinking how mitochondrial and Y-chromosome techniques of population genetic analysis have paved the way for multiple forms of belonging. One crucial development concerns the shifting meanings of the genetic or evolutionary family. As the discourses surrounding Mitochondrial Eve indicate, there is a shift from the idea of a global human family that we all belong to through our shared molecular kinship toward biotechnological practices and cultural rhetoric that locate kinship ties on increasingly small entities such as regional populations, haplogroups, or imagined prehistoric clans. This development has generated a growing interest in the genetic roots of nations and ethnic communities.

Another key development stems from mitochondrial and Y-chromosome technologies' focus on molecular lineages. This linearity resonates with attempts to locate personal or communal roots deeper in the past and to render those roots precise and irrefutable. In particular, it resonates with national narratives' engagement with linear historical trajectories. National narratives typically seek to establish the nation as an ontologically necessary entity by emphasizing national origins and destinies. The idea of direct genetic lineages provides a powerful tool for

imagining an irrefutable connection between the present nation and a seemingly authentic, foundational past. The assumption of purity associated with direct lineages supports this dynamic. Commenting on the study of Irish Y chromosomes introduced at the beginning of this chapter, Nash (2006) problematizes the idea of genetic purity: "[w]hen translated into genetic measures of who is 'most Irish of the Irish', population genetics is enmeshed in the most potent politics of sovereignty, identity, and citizenship" (Nash 2006, 19). While Nash discusses Y-chromosome ancestry, her point also applies to mitochondrial ancestry, as both technologies rely on a logic that excludes genetic, cultural, political, and linguistic ties that do not follow a uniparental pattern of genetic transmission.

The connections between mitochondrial and Y-chromosome techniques and the affective politics of gender, sexuality, and race traced in the chapter imply that the emerging forms of belonging are also packed with gendered, sexualized, and racialized meaning. The debates surrounding Mitochondrial Eve and Y-Chromosome Adam suggest that these meanings cannot be easily undone. Rather, mitochondrial and Y-chromosome technologies, assumptions of gendered and racialized difference, and ideas of belonging are intertwined so that they shape one another. The following chapters will explore the role of gender, sexuality, and race in these emerging configurations of belonging. Narratives of belonging have always been invested in issues of reproduction, whether the symbolic reproduction of the community or nation, or the literal reproduction of its members or citizens. Accounts of mitochondrial and Y-chromosome inheritance often reinforce this reproductive focus by invoking a language of temporal linearity that ties gender, sexuality, and race to biologized continuity. Similarly, the way in which the structural parallelism of mitochondrial and Y-chromosome technologies resonates with heteronormative assumptions renders the new genetically framed modes of belonging structurally gendered, as if the history of the community or nation consisted of two parallel yet intimately linked male and female histories, which come to stand for the promise of reproduction and thus futurity. While such heteronormative undertones are by no means new, the epistemic authority widely ascribed to genetic discourse

naturalizes cultural assumptions about two binary and complementary genders.

While these emerging configurations of belonging build on a long tradition of imagining the roots and destinies of communities, nations, and individuals, the analytical techniques of population genetics invest them with particular affective appeal: they promise to discover "deep" ancestry instead of the more recent roots documented in historical records. This results in a shift in the affective politics of belonging. The integration of population genetic discourse into imaginaries of belonging enacts a move toward an idea of inner personal, communal, or national identity, invisible to the naked eye but open to new sequencing technologies and the scientists' high-powered microscope. The way in which mitochondrial and Y-chromosome techniques highlight linearity also gives the emerging forms of belonging a sense of promised continuity. In this, they serve to appease concerns about the future of the community that have always haunted narratives of national or communal unity. Population genetics carries considerable affective appeal since it provides answers that are always multiple: depending on the statistical methods, computer programs, and level of analysis used in inquiry, population genetics provides different answers to questions of belonging. Yet those answers tend to appear as the single, ultimate truth. Such a conjoiner of flexibility and authority fits well within contemporary accounts of belonging, which often seek to urgently respond to changes in ethnic relations or national boundaries. From this blurriness and multiplicity arises a new kind of ambiguous essentialism suitable for the twenty-first century.

Notes

1. These distinctions were not watertight though: commenting on the 2009 study of mitochondrial DNA from human fossils on the deCODE website, the company's CEO Kári Stefánsson suggested that such studies have significance beyond the national context by shedding light on "the history not just of single populations, but of our species and how we spread from Africa to every corner of the globe" (deCODE Genetics 2009).

2. For the Icelandic case, see, for example, Greely (2000), Greenhough (2006), Pálsson and Harðardóttir (2002), Pálsson and Rabinow (1999), Rose (2003), Winickoff (2003). For the Irish case, see especially Nash (2006).
3. The neutral model was also largely compatible with the theoretical models of variation by Lewontin and Hubby (1966) (Suárez and Barahona 1996, 70).
4. Most of the media texts discussed in this and following sections were located through the LexisNexis database using "Mitochondrial Eve" as a search term.
5. For population geneticists' attempts to negotiate ideas of race and population-level difference, see Jenny Reardon's *Race to the Finish* (2005).
6. For a celebration of African origins inspired by Mitochondrial Eve, see, for example, author and poet Aurora Levins Morales's text "African Creation," published in the journal *Callaloo* in 1994 (Morales 1994).
7. Some of these complexities are given voice in media texts on the implications of the theory of Mitochondrial Eve for the place of the British in evolutionary history. For example, molecular geneticist Johnjoe McFadden writes in the British paper *The Guardian* in 2001 that the popular idea of "British genes" is unsubstantiated, that "we are all African immigrants" descended from Mitochondrial Eve, and thus "[w]e are all mongrels and should be proud of it," thereby questioning the assumption of Anglo-Saxon privilege (McFadden 2001). Some accounts demonstrate inherently contradictory tendencies, as when a 2012 piece in *The Telegraph* tells the story of a Scottish lecturer whose mitochondrial DNA is revealed to be remarkably closely linked to the mitochondrial haplotype of Mitochondrial Eve. The text quotes researchers involved in the tests describing the teacher as a "thoroughbred" and the "grandson of Eve, or the grandfather of everyone in Britain," while stating that the result "is further proof that even white Anglo-Saxon protestants are descended from a black Eve" (Cramb 2012).This portrayal appears to simultaneously establish Anglo-Saxon privilege and to question it.
8. Catherine Nash (2012, 2015, 137–169) sees this theoretical alliance between population genetics and evolutionary psychology as a growing tendency in population genetics.
9. Sarah Wilcox (2003) provides an interesting discussion of the cultural embedding of science news in the context of the scientific study of homosexuality.
10. The coupling of Mitochondrial Eve and Y-Chromosome Adam finds another related parallel in the image of the universal human family that

Donna Haraway (1997) connects to the scientific idea of population. Reflected in such postwar cultural documents as the 1955 "Family of Man" exhibition, the reproductive heterosexual nuclear family appears to celebrate human difference while in fact reproducing what Haraway calls a "grammar of indifference, of the multiplication of sameness" (Haraway 1997, 243).

11. The connection between biotechnologies and visions of a better future has been noted by a number of scholars. See, for example, Borup et al. (2006), or Bloomfield and Doolin (2011).
12. For an overview of the uses of affect and emotion in feminist affect studies, see Gorton (2007).
13. For discussion of gender and sexuality in genetic kinship, see also Catherine Nash (2005, 2012) and Catherine Lee (2012).
14. For the reproductive logic of evolutionary narratives, see Roof (2007), Turner (2007), Wald (2000), or my *Gender, Sexuality and Reproduction in Evolutionary Narratives* (2013).
15. This resembles the logic that Laura Briggs and Jodi I. Kelber-Kaye (2000) identify in Michael Crichton's 1990 science fiction novel *Jurassic Park*. While focusing on nuclear DNA rather than mtDNA, the novel posits the nuclear family as the only possible defense against chaos and destruction caused by attempts to clone dinosaurs from ancient DNA. In the novel, the absence of males in both human and dinosaur reproduction constitutes a threat to order, while gender nonconformity and feminism appear as dangerous aberrations that will be punished with death.
16. Bryan Sykes's (2001) aforementioned book *The Seven Daughters of Eve* is a good example of this phenomenon.

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3

Imagining Origins Through Ancient Human DNA

Belonging is a temporal dynamic that locates us within historical processes of transformation and gendered and racialized relations, as the debate about Mitochondrial Eve in the previous chapter suggested. In the case of human population genetics, this temporal dynamic engenders connections between us—the affective subjects—and the reconstructed evolutionary continuum reaching from the prehistoric African savannah to the complexities and confusions of modern life. It is hardly surprising that attempts to imagine belonging in public discourse often center on roots, a point of origins for the imagined community that we presumably belong to. Such a point of origins is important for belonging because it appears to establish the imagined ethnic, racial, regional, or national community as temporally primary to other communities with shorter histories.

The means of imagining roots have transformed with technological and cultural change. Science has played a key role in these developments. Crucially, the age of national romanticism in nineteenth-century Europe was also an age of scientific innovation and progress, as fields of study such as geology, evolutionary theory, comparative anatomy, and anthropology

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increasingly claimed epistemic authority over realms of knowledge previously governed largely by folklore, mythology, or religious philosophy. This parallel development of new forms of imagining national, ethnic, and racialized communities and new forms of science materialized in the growing institutional and public interest in the paleontological study of ancient hominin remains. While hominin fossils were seen as providing insight on human evolution in general, they were also interpreted and endorsed as evidence of the prehistoric roots of the modern people who resided in the region where the remains were discovered.

By the early twentieth century, discoveries of ancient remains were still rare. The most famous hominid specimens included the first Neanderthal fossil discovered in Feldhofer Cave in Neander Valley in Germany in 1856 (Goulden 2009) and a Neanderthal skull found in the French village of La Chapelle-aux-Saints in 1908 (Sommer 2006; Goulden 2009; Pyne 2016), as well as the "Java Man" *Homo erectus* fossils discovered on Java in Indonesia in 1891–1892 (Puech 1983; Storm 2012; Swisher et al. 2002), and the "Peking Man" *Homo erectus* fossils discovered in China from 1929 onward (Sautman 2001; Leibold 2006; Pyne 2016). These fossils played a key role in debates about the evolution of modern humans by operating as "missing links," that is, as intermediate forms between humans and apes. At the same time, they were immersed in politically charged debates about social order, racial hierarchies, and national and ethnic identities. In his study of the political uses of the Peking Man fossils in China in the 1990s, Barry Sautman (2001) aptly calls the conjoiner of paleontology and nationalist discourse "paleoanthropological nationalism." The party-led attempts to establish China as the birthplace of a presumably unique advanced hominid, and the said hominid as the true ancestor of the Chinese rather than as an extinct species, represent, of course, an extreme form of paleoanthropological nationalism. Yet similar nationalist striving has influenced a number of attempts to explain hominin fossils discovered in Europe in the nineteenth and twentieth centuries.

The discovery known as "Piltdown Man" demonstrates clearly how ancient hominin remains have operated as means of claiming national or racial supremacy. Piltdown Man was not a genuine fossil but a combination of human cranium and an orangutan jawbone, which were stained

to give them a strikingly old appearance. Discovered in a gravel pit in Piltdown, East Sussex, in 1912, Piltdown Man was taken as the real thing by British scientists for four decades until 1953. In his insightful analysis of the hoax, science studies scholar Murray Goulden observes that the Piltdown fossil was seen as "provid[ing] England with an ancient history to match those of imperial rivals France and Germany," which were already able to claim great ancestry through the Neanderthal finds within their national borders (Goulden 2009, 288). Furthermore, the Piltdown discovery resonated nicely with Britain's reputation as the birthplace of modern evolutionary theory. Goulden suggests that scientists were so eager to overlook the species ambiguity of the Piltdown remains because "Piltdown the earliest Englishman was far more appealing than Piltdown the earliest English ape. … In fact, such was their keenness that no questions were asked of Piltdown upon its arrival, it was simply waved through the checks that one might expect" (Goulden 2009, 285). This framing of Piltdown Man as both human and English organized, for example, leading Piltdown scientist Sir Arthur Smith Woodward's account of the discovery, *The Earliest Englishman*, published in 1948, five years before the hoax was exposed. Significantly, the nationalist framing also invoked racial differences: Piltdown Man was compared to indigenous populations with the result that Piltdown Man became human, while indigenous people were moved simultaneously further away from modernity through their resemblance to Piltdown Man (Goulden 2009, 277). This suggests that fossils identified as intermediate hominid species provided an appealing affective resource for those wishing to promote the antiquity of the national community through claims of inevitable racial hierarchies.

Since the early twentieth century, the number of discovered hominin fossils has grown considerably, engendering important knowledge on human evolution in different geographic locales around the world. At the same time, new methods of studying prehistoric bones have emerged. In particular, the development of techniques of genetic analysis of fossilized remains—*paleogenetics*—has opened up early human evolution as a molecular process. The previous chapter showed how mitochondrial DNA (mtDNA) analysis emerged as the first major genetic tool for untangling the geographical diversity of modern humans and their

historical relatedness. In this light, it is not surprising that mtDNA analysis played a crucial role also in the development of ancient DNA (aDNA) analysis, especially as it is the type of DNA most likely to have survived in old and poorly preserved bones. Following technological development, however, Y-chromosome analysis and, more recently, advanced genome sequencing techniques have been used to flesh out and complicate the picture of human evolution achieved through analysis of ancient mtDNA.

A crucial part of the paleogenetic approach is the comparison of ancient and modern DNA. The significance of this conjoiner of two sources of genetic material, past and present, is often highlighted in popular discourse. For example, popular science writer Matt Ridley suggests that information about the past "can be inferred from the study of modern DNA, but ancient DNA can catch it in the act" (Ridley 2015). Similarly, geneticist and popular science writer Bryan Sykes states that "[a]s a witness to the past events we have the DNA of living people, which is technically straightforward to analyze but can be hard to interpret, and the DNA of the dead, which is very difficult to work with but considerably easier to interpret" (Sykes 2012, 19). Furthermore, echoing the tradition of framing ancient human remains within nationalist or regionalist narratives, DNA retrieved from ancient bones is often invoked in the context of ethnic or national roots. As recently as in the spring 2015, aDNA collected form prehistoric human remains found in the Basque country was celebrated for probably having "solved the puzzle of one of Europe's most enigmatic people: the Basques" (BBC News 2015).

The use of ancient DNA to imagine, define, and narrate national, regional, and ethnic forms of belonging is the topic of this chapter. While the previous chapter traced the affective debates surrounding the emergence of mitochondrial and Y-chromosome analyses, the current chapter focuses on the role of mitochondrial, Y-chromosome, and genome-wide sequencing techniques in the study of human fossils. The chapter asks what happens when those fossils become a source of ancient DNA, which is then compared and connected to contemporary DNA within modern-day populations. That is, how are the roots of genetic communities—national, racialized, ethnic, regional—enacted through comparisons between ancient and modern DNA? What kinds of tensions and resonances emerge between these forms of belonging?

Continuing the discussion on the connections between genetic technologies and categories of difference in the previous chapter, I explore how paleogenetic uses of mitochondrial, Y-chromosome, and genome-wide techniques invoke and refashion gender, race, and class. I connect these shifting articulations of intersecting differences to the affective appeal of establishing the roots of national, regional, or ethnic communities through ancient DNA. I show how paleogenetic studies of human ancestry have provided accounts of national, ethnic, and regional antiquity with powerful rhetorical resources by making roots appear as material, affective, as well as suggestive of differences that can be drawn upon to establish boundaries for the community. As these rhetorical resources can be invoked in multiple, mutually contradictory ways, they may enact several competing forms of belonging and difference.

The chapter begins with an account of the introduction of the genetic analysis of hominin fossils, especially the role of mitochondrial analysis, and the shift toward genome-wide analysis in the past decade. The following sections explore the interplay between different forms of belonging in two national contexts: the United States and the United Kingdom. First, I discuss the role of ancient human remains in the construction of US national narratives and both Native American and Euro-American configurations of roots and belonging. What makes the US national narrative particularly intriguing is the relative shortness of national history, and the rhetorical dilemma of separating American history form European history while also recognizing the existence of Native Americans on the continent thousands of years prior to the birth of modern nation-states. I analyze the cultural and scientific debate surrounding the 9000-year-old remains known as Kennewick Man discovered in Washington State in 1996. The Kennewick remains became an object of an intense and highly affective debate concerning ownership of prehistoric human remains, epistemic authority over prehistory, and prehistoric racial categories. At the same time, the Kennewick remains demonstrate central tendencies underlying the scientific and cultural role of ancient human DNA: the remains played a crucial part in the debate about what genetic analysis could offer for the study of national, regional, or ethnic prehistory from the moment of their discovery nearly two decades before the Kennewick DNA was finally successfully sequenced in 2015.

Second, I investigate the role of ancient human DNA in the construction of national, regional, and personalized forms of belonging in the United Kingdom. While Britain has been able to claim a longer national history than the United States, British history is also characterized by complexities, as the isles have been occupied by a number of populations including the Picts, Celts, Romans, Vikings, Saxons, and Normans. My analysis focuses on Cheddar Man, the first complete prehistoric skeleton discovered in the United Kingdom. Found in Cheddar Gorge in Somerset in 1903, the remains were subjected in 1996 to genetic analysis, which claimed to connect the mtDNA extracted from Cheddar Man's molar to a local schoolteacher. The ensuing public debate invoked ideas of straightforward evolutionary trajectories that erased the complexities associated with existing knowledge of British history. It also cherished the idea of national, regional, and personal roots as preserved within our cells rather than in historical documents, oral traditions, or archeological artifacts.

The final sections of the chapter develop two key themes invoked in the scientific and public debates surrounding the Kennewick and Cheddar remains. One of them is the assumption that national and ethnic roots reside within us. This renders the connection to the past as highly intimate and emotionally charged, always present and alive wherever we are. Yet this imagined concrete materiality is ambivalent: what makes the concreteness of roots recorded in DNA possible is the fact that significant parts of our DNA are shared across the very same evolutionary continuum that is being invoked to identify differences between individuals and populations. The second theme is the idea that genetic analysis of ancient human remains renders communal roots a specific kind of affective space. I elaborate on how the widely endorsed connection between ancient and modern DNA places this mythic space within a culturally resonant temporal dynamic, opening it up to multiple modes of belonging.

The Emergence of the Study of Ancient Human DNA

The previous chapter traced the emergence of mitochondrial and Y-chromosome analyses as means of imagining human prehistory from the late 1980s through the 1990s. The analysis of aDNA explored in this

chapter is part of the same series of technological and theoretical innovations. While Cann, Stoneking, and Wilson's 1987 mitochondrial paper used contemporary mitochondrial variation as a basis for evaluating key patterns of human evolution, the study of aDNA turned to a different type of mitochondrial material: mtDNA retrieved from fossils, mummified remains, museum specimens, and archeological sites. Two early important cases involved mtDNA extracted from the dried muscles of a 140-year-old quagga (an extinct species related to zebra) by Russell Higushi and colleagues in 1984 (Higuchi et al. 1984), and mtDNA retrieved from an Egyptian mummy by Svante Pääbö in 1985 (Pääbo 1985). These studies were conducted without the help of polymerase chain reaction (PCR), the amplification technique developed by Kary Mulligan in 1983, which allowed scientists to use ever-smaller and less well-preserved segments of DNA by amplifying genetic material seemingly endlessly. While this was important for the rise of population genetic studies of contemporary mtDNA in the late 1980s and early 1990s, it was particularly important for aDNA studies, as ancient samples tend to be in poor condition.

The reasons why aDNA studies began with the analysis of mtDNA were largely the same as why population genetic studies focused on contemporary mtDNA in the 1980s and early 1990s. Mitochondrial DNA was present in multiple copies in each cell, and it was also considerably shorter than nuclear DNA. This made its analysis less complicated than the analysis of nuclear DNA (DNA located in the chromosomes in the cell nucleus), or the analysis of *autosomal* DNA (nuclear DNA minus X and Y chromosomes). Inherited from only one parent, the information it provided was easier to turn into evolutionary trees or *phylogenies* than that provided by recombining nuclear DNA. Furthermore, what made mtDNA attractive for aDNA studies is its slower rate of degradation compared to nuclear DNA. Thus, with very old samples, mtDNA was often the only thing left for analysis. It is not surprising, then, that mtDNA has been, as anthropologist Connie J. Mulligan puts it, "the molecule of choice in aDNA studies" (Mulligan 2006, 369; see also Rizzi et al. 2012, 3; Anastasiou and Mitchell 2013, 29). In the mid-1990s, mitochondrial analysis was applied successfully to several ancient hominid specimens. In 1994, geneticist Oliva Handt and colleagues reported the initial results of mtDNA retrieved from Ötzi the Iceman,

the 5000-year-old natural human mummy discovered in the Alps in 1991 (Handt et al. 1994). In 1997, geneticist Matthias Krings and colleagues announced that they had analyzed an mtDNA sequence extracted from the famous Neanderthal remains found in Feldhofer Cave, Germany, in 1856 (Krings et al. 1997; see also 1999). While these studies were able to analyze only short sections of mtDNA, their results suggested that, with future technical development, aDNA could potentially answer previously unsolved questions about human evolution.

The affectively charged debate about Mitochondrial Eve and human origins provided a context within which the study of ancient mtDNA was also sometimes framed. In a 1993 overview of the impact of "biomolecular archaeology" on archeology, archeologist K. D. Thomas invokes this framing by suggesting that although "[s]o far the rather limited and scattered results of biomolecular archaeology have not led to conflicts with archaeologists … those concerned with the origins of the earliest human beings will be aware of the great controversies existing between (some) molecular geneticists and (some) physical anthropologists" (Thomas 1993, 2). Ten years later, biological anthropologist Dennis H. O'Rourke is ready to conclude that "the aDNA data appear to provide less support for multiregional evolution than for a single, recent origin" of modern humans, an evaluation that echoes the growing acceptance of the mitochondrial and Y-chromosome phylogenies produced within population genetics throughout the 1990s (O'Rourke 2003, 106). Yet O'Rourke cautions that "[t]he reality of our evolutionary history may be less clear-cut. If, for example, modern *Homo sapiens* originated in Africa, and during migrations to other continental regions interbred with existing archaic populations, the distinctions between the replacement and multiregional models become blurred, and the predictions about patterns of genetic variation based on such models also become more complex" (O'Rourke 2003, 106). This suggests that the affectively charged juxtaposition between single-origin and multiple-origin theories in the first decade of population genetic analysis of mtDNA was beginning to acquire increasingly nuanced and complex tones with the technological and theoretical developments of the new millennium.

Many of the scientists working in related fields such as paleoarcheology or paleoanthropology welcomed aDNA analysis with both curiosity

and reservations. Writing to other archeologists in 1993, K. D. Thomas, for example, acknowledged archeologists' potential reservations about molecular methods while nevertheless predicting that "[b]iomolecular archaeology has great potential and it will be fascinating to track its development" (Thomas 1993, 13). Outside professional science, the first studies of ancient mtDNA were met with enthusiasm, which gained further momentum in the early 1990s following the announcement of a number of amazing analyses of mtDNA extracted from long-extinct species. These claimed discoveries even included dinosaur DNA, a theme reflected in Michael Crichton's 1990 bestselling novel *Jurassic Park* and its 1993 film adaptation.

Much of the appeal of aDNA studies among scientists as well as the public arose from the prospect of comparing ancient and modern mtDNA. Writing in 1999, biologists Robert K. Wayne, Jennifer A. Leonard, and Alan Cooper suggested that "[a]ncient DNA analysis can provide a direct record of the tempo and mode of genetic change within populations, and thus a means of testing and refining existing population models" (Wayne et al. 1999, 469). Similarly, anthropologist John H. Relethford states in 2001 that with the help of aDNA analysis, "[i]nstead of having to base all of our genetic analyses on a single point in time (the present) we have the potential to examine temporal as well as spatial changes" (Relethford 2001, 390). Thus, "[s]tudies of living human mtDNA can be useful in addressing recent evolution, but ancient mtDNA is needed to extend our interpretations further into the past" (Relethford 2001, 391).

The study of aDNA, then, was seen as providing a unique viewpoint to the temporal dynamics of human evolution. This uniqueness arose from the ability of aDNA to shed light on now-extinct lineages that cannot be traced through modern samples, as modern samples only include surviving lineages. By comparing ancient and modern DNA samples, scientists are able to view evolutionary processes through two distinct moments in history, thereby building fuller and more accurate genetic genealogies than those engendered through extrapolation from modern genetic diversity alone. Ancient DNA studies were understood to provide not just a look into a moment in the past but a temporal trajectory, an account of how we became us. Furthermore, the analysis of aDNA was also associated

with direct, unmediated access, as suggested by Wayne and colleagues' mention of "a direct record" above (Wayne et al. 1999, 469), or by Mulligan's 2006 portrayal of aDNA studies as offering "an opportunity to *directly* investigate the genetic makeup of past populations" (Mulligan 2006, 377; emphasis mine).[1] While aDNA certainly had potential to generate a more detailed view of the evolutionary past than modern DNA could, invocations of direct access to the past are somewhat misleading: aDNA engenders knowledge about human evolution only through complex mathematical and statistical models used also in the analysis of modern samples. Yet the idea of direct access and unmediated knowledge is powerful: indeed, it is a central feature of my two case studies, the debates surrounding the Kennewick and Cheddar remains.

In the mid-1990s and early 2000s, the revelation of several technical problems in aDNA analysis shifted the atmosphere surrounding aDNA from excitement to caution. First of all, the most impressive discoveries involving million-year-old DNA were revealed to be results of contamination by modern human DNA. Contamination turned out to be a major methodological problem. Practically all old samples had been handled by excavating archeologists, museum workers, and scientists themselves, who had potentially left their DNA on the specimens. Furthermore, while PCR had made the analysis of scarce DNA material possible by amplifying it, the use of PCR had also inadvertently contributed to the problem of contamination: PCR tended to amplify well-preserved contemporary DNA rather than the fragile, poorly preserved ancient DNA. Second, the inevitable degradation of DNA over time meant that DNA retrieved from prehistoric samples often demonstrated considerable damage to the original sequence. For example, miscoding lesions in the DNA sample would cause base substitutions—typically the replacement of G (guanine) with A (adenine), or T (thymine) with C (cytosine)—which, if unidentified, generated an incorrect reading of the ancient sequence. These problems led to the establishment of strict guidelines for all aDNA studies (Cooper and Poinar 2000).

These technical challenges encouraged a careful tone in scientific overviews of aDNA studies around the millennium. While generally optimistic about the field, Wayne, Leonard, and Cooper nevertheless refer to "[t]he rise and decline of ancient DNA research" (Wayne et al. 1999, 468),

noting that "[t]he number of ancient DNA papers has declined in the past few years as has the number of reports appearing in high profile journals. … The honeymoon period has passed for ancient DNA research, and the difficulties associated with a maturing field need confronting" (Wayne et al. 1999, 464). In a similar vein, Svante Pääbö, one of the leading researchers working on aDNA at Max Planck Institute for Evolutionary Anthropology, writes with his colleagues: "To enthusiasts, it once seemed that there was no limit to what could be achieved when the PCR was applied to ancient remains…. In our opinion, it is likely that all million-year-old DNA sequences are artifacts" (Pääbo et al. 2004, 661). According to Pääbo and colleagues, "[t]he study of ancient DNA sequences has had relatively limited impact on our understanding of recent human history, and this situation is unlikely to change in the near future" (Pääbo et al. 2004, 664). Despite considerable successes such as the analysis of mtDNA from the Neanderthal remains and Ötzi the Iceman, the technical limits of ancient mtDNA analysis had cast aDNA in a supporting rather than leading role in the study of human evolution by the early years of the new millennium.

From mtDNA to Nuclear DNA

The study of aDNA experienced a new boost around 2005. The push came from the development of new sequencing technologies that enabled the simultaneous analysis of several DNA sequences in a single run. The so-called Sanger technique used until this point had been slow, or "low throughput," and its use had been limited to short sequences. The new sequencing technologies, known as Next Generation Sequencers, were fast, efficient, and increasingly accurate, and thus "high throughput." These new technologies made it possible to analyze complete DNA sequences: the costs were feasible for established and well-funded labs, and the advanced methods allowed the analysis of large and complex data. These developments engendered a quick succession of impressive results within aDNA studies. In 2008, the entire mitochondrial genome of the Tyrolian Iceman Ötzi was sequenced (Ermini et al. 2008), as was the entire Neanderthal mitochondrial sequence (Green et al. 2008). In

2010, the first ancient nuclear genome was analyzed (Rasmussen et al. 2010): the DNA was retrieved from 4000-year-old human hair preserved in permafrost in western Greenland. In the same year, Pääbo's lab published the draft sequence of the Neanderthal nuclear genome (Green et al. 2010), as well as the mitochondrial genome of the Denisovan, the extinct hominin species discovered recently in Siberia (Krause et al. 2010), followed by the publication of the Denisovan draft nuclear sequence (Reich et al. 2010). What made the Denisovan case particularly interesting was that the evolutionary history of an entire hominin species was constructed from a small sample of genetic material. As Ermanno Rizzi and colleagues note, "[i]n fact, at present, except for the phalanx [finger bone] and a tooth retrieved during the archaeological excavation, no other physical and morphological feature of this population is known" (Rizzi et al. 2012, 14).

Not surprisingly, these considerable successes were met with celebration, engendering a forward-looking ethos among the scientists and the public. The following quote from the news section in the journal *Nature* in 2011 captures this affective shift:

> For a field that relies on fossils that have lain undisturbed for tens of thousands of years, ancient human genomics is moving at breakneck speed. Barely a year after the publication of the genomes of Neanderthals and of an extinct human population from Siberia, scientists are racing to apply the work to answer questions about human evolution and history that would have been unfathomable just a few years ago. (Callaway 2011, 136)

Similarly, George H. Perry and Ludovic Orlando, editors of a 2015 *Journal of Human Evolution* special issue on aDNA, declare that "it is clear that feats previously considered impossible have now been achieved" (Perry and Orlando 2015, 1), and in an article published in the same issue, Luca Ermini, Clio Der Sarkissian, Eske Willerslev, and Orlando announce that "[a]ncient DNA research has now come of age" (Ermini et al. 2015, 5). The tone is distinctly future-oriented, as when Perry and Orlando remark that "[w]e are in the midst of a true revolution in ancient DNA research" (Perry and Orlando 2015, 1), and Ermini and colleagues write that "[g]iven recent methodological developments, we can confidently predict that this is only the beginning" (Ermini et al. 2015, 14).

Crucially, this technical revolution does not involve only the efficiency of genetic analysis but also the kind of knowledge that can be achieved. As the Neanderthal and Denisovan studies suggest, one key shift has been the move from mitochondrial analysis to the analysis of the nuclear genome. This, in turn, has shifted the scientific (and public) gaze from the noncoding genetic variation suggestive of evolutionary descent to the genetic detail suggestive also of phenotypic expression—that is, what the ancient hominins looked like. For example, the 2010 study of the hair preserved in permafrost in Greenland provided an estimate of several physical features, including hair color, metabolism, and body mass index, based on the analysis of autosomal DNA—that is, nuclear DNA excluding the X and Y chromosomes—and knowledge about environmental factors (Rasmussen et al. 2010).

One result of this shift from mtDNA to nuclear DNA has been the realization that different methodologies and technologies engender different evolutionary histories. For example, the analysis of the Denisovan and Neanderthal mitochondrial genomes suggested that Neanderthals and modern humans were "sister groups," while Denisovans diverged from both about one million year ago. However, the analysis of Denisovan and Neanderthal nuclear genomes suggested otherwise: Denisovans and Neanderthals were sister groups, while modern humans had diverged from both of them some 800,000 years ago. As geneticist Carles Lalueza-Fox points out, the problem was that the prehistoric lineages connecting a particular type of genetic material (mtDNA) were taken as representing the history of the species as a whole (Lalueza-Fox 2013, S216). In the same way, the mitochondrial genome of Neanderthals had suggested that Neanderthals did not interbreed with humans (Green et al. 2008), but the nuclear Neanderthal genome indicated a certain level of interbreeding (Green et al. 2010). Again, these conflicting findings were the result of focusing on different types of genetic material. What favored nuclear DNA in most scientists' view was its large number of genetic markers and its inheritance from a range of ancestors rather than through one line of descent. This made the nuclear genome a "more informative" and reliable witness to the past than mtDNA (Rizzi et al. 2012, 15). With the development of advanced sequencing techniques, then, what had earlier appeared as a strength (small size and uniparental inheritance) now

appeared as a weakness. This makes Lalueza-Fox announce that "[t]he scientific time of the mtDNA and Y chromosome as the main tool to correlate with the fossil record is coming to an end" (Lalueza-Fox 2013, S216), a sentiment echoed by many other scientists (e.g. Rizzi et al. 2012; Anastasiou and Mitchell 2013; Hofreiter 2015).

This shift from mitochondrial analysis to genome-wide analysis of nuclear DNA will be reflected on throughout this book. I will focus on the different dynamics of belonging that arise from the shifts between these analytical techniques. While nuclear DNA has opened up new possibilities of building more complex and detailed phylogenies, mtDNA still informs ideas of genetic belonging because it has directed the scientific search for human evolutionary history for so long. Indeed, as biologist Michael Hofreiter and colleagues point out, "[t]he emphasis on mtDNA that has persisted in aDNA research for a long time has almost certainly influenced the way researchers have thought about evolutionary history" (Hofreiter 2015, 288). At the same time, Hofreiter and colleagues highlight how nuclear sequencing is changing how we understand the human evolutionary past previously studied through mtDNA:

> Contrary to mtDNA, the nuclear genome represents thousands of recombining loci, under varying selection intensities, and will therefore better reflect the complex and gradual nature of evolution… Thus, rather than representing distinct independent entities, populations should be seen as open pools connected to other pools by larger or smaller rivers. … Extant populations are therefore the product of a complex and dynamic history of connections and separations that may not fit the convenient categorical model suggested by mtDNA. (Hofreiter 2015, 289)

Whereas mtDNA (and other uniparental entities like Y-chromosome DNA) foregrounds exclusion—your mtDNA either is or is not descended from a particular ancestor—the nuclear genome provides a view of descent that recognizes mixing and the blurriness of population boundaries. Crucially, both conceptualizations have considerable affective appeal across a range of social, cultural, political, and ideological positions, as I will argue in Chap. 5.

Narrating American Roots

The United States has a complicated relationship to early history. The US national narrative is characterized by shortness compared to many other countries, spanning only a few hundred years, often identified with the arrival of the Mayflower. At the same time, the population of the United States has long been one of the most diverse ones in the world—as it is often phrased, the United States is a nation of immigrants. While genetic testing of *individual roots* is highly popular in the United States, the overall genetic makeup of the American population is considerably complex and diverse, and, for that reason, not considered generally as particularly interesting. Not surprisingly, ethnically or racially defined genetic projects such as Howard University's 2003 decision to open an African-American biobank, *Genomic Research in the African Diaspora* (GRAD), appears to have attracted more popular attention than attempts to capture the overall genetic variation of the nation. In fact, the very idea of an "American genome" is difficult to envision. This is suggested, for example, by the structure and rhetoric of the British geneticist Bryan Sykes's 2012 popular science book *DNA USA: A Genetic Portrait of America*. While Sykes has previously produced popularly appealing narratives of the genetic foundation of Europe in *The Seven Daughters of Eve* (2001) and the people of Great Britain and Ireland in *Blood of the Isles* (2006; published in the United States as *Saxons, Vikings, and Celts*), *DNA USA* differs considerably from these books. The first half of the book focuses on populations outside the United States, including British and Scottish history, Jewish diaspora, and African diaspora, and the narrative appears to struggle to produce a vision of uniquely American inheritance. This is, I believe, indicative of the difficulties of incorporating genetics into an American national narrative in a way that would focus the narrative on a common, unifying descent.

Considering the relatively short history of the United States as a nation, it is not surprising that both scientific and popular attention has often focused on the first inhabitants of the North American continent—that is, the prehistoric arrival of the so-called Paleo-Indians. The appeal of this focus is twofold. The focus on Paleo-Indians provides a temporal scope

absent in narratives of the birth of the American nation. It also highlights the unity of human origins on the North American continent and thus presumed genetic homogeneity by focusing on an apparently clearly defined population that precedes European contact. It is important to note that this interest in the Paleo-Indian past is not a product of the age of genetics. The prehistory of the American continent has preoccupied European colonists ever since their arrival and first encounter with Native Americans. The presence of Native Americans in North America thousands of years before the European colonists should have logically posed major problems for any attempt to embed the US national narrative within the prehistory of the continent. Yet the historical primacy of Native Americans was turned and twisted in scientific and public discourse in ways that served various political ends.

Annette Kolodny has shown that eighteenth- and nineteenth-century Euro-American accounts of American history were dominated by two mutually exclusive yet persistently coexisting theories about the role of Native Americans in the prehistory of the continent (Kolodny 2003). On the one hand, Native Americans were portrayed as prelapsarian figures located outside history, as if time only began with the arrival of Columbus and the European colonists in 1492. This narrative strategy cast Native Americans as eternal children who simply did not have the means to survive in a civilized world and therefore were destined to disappear. On the other hand, there was a growing conviction among commentators that the elaborate cultural artifacts discovered at ancient burial sites were designed by a now-lost Old World civilization. This "Mound Builder" myth rendered Native Americans barbaric sinners who had destroyed the original civilization, and therefore deserved to be removed from their lands (which, the myth insisted, were not theirs in the first place). This narrative framing rendered Native Americans as neither ancient nor civilized (Kolodny 2003; Howey 2010).

Yet the Euro-Americans' discursive and epistemic triumph was not complete. The Euro-American view of writing as a sign of true communal existence renders prehistory a distant, blurry territory. Native American narratives, by contrast, highlight oral tradition, which sees knowledge as a product of an uninterrupted historical continuum. In her exploration of nineteenth-century Native American histories, Meghan C. L. Howey

(2010, 437) notes that many Native American authors insisted that what the Euro-Americans saw as a "puzzle" of Native American origins (and hence prehistory) was not a puzzle for the Native Americans. What complicates the picture further is that many Native American communities have collected and integrated paleontological evidence—fossilized animal bones, for example—into their accounts of prehistory, as Adrienne Mayor (2005) demonstrates. Native American accounts of origins, then, do not necessarily operate in strict opposition to the methods and purposes of science, but rather tread on the same cultural and epistemic territory.

New discoveries of archeological and paleontological evidence during the twentieth century began to fill in the picture of the prehistory of the continent, correcting some of the openly racist assumptions made by the early Euro-American commentators. The discoveries of stone tools at sites near Clovis, New Mexico, in the 1920s and 1930s gave rise to the view that all indigenous peoples in the Americas are descended from a single culture (called Clovis after the discovery site) that had arrived across the Bering land bridge from Siberia some 12,000 years ago. This "Clovis first" hypothesis was questioned in the 1990s, after an expert panel determined that an archaeological site discovered in Monte Verde, Chile, in 1977, indeed predated Clovis culture (Dillehay 2000; Jablonski 2002). This opened the debate for different theories of when the human colonization of the continent took place, with estimates ranging roughly between 40,000 and 10,000 years before present. Scientists have also provided different theories of the number of waves in which the Paleo-Indians arrived, how the different waves were connected genetically, where on the American continents each wave of immigration eventually spread, and whether the first Americans traveled on foot or used rudimentary boats.[2] Another central question has concerned the places of origin in Asia for the prehistoric migrations to America.

In the 1990s, population genetics entered the debate about American prehistory. Using the newly developed techniques of analyzing mitochondrial and Y-chromosome DNA, geneticists analyzed DNA samples from contemporary Native American and Asian populations. These research projects built on the same theoretical framework as the search for Mitochondrial Eve and Y-Chromosome Adam explored in the previous

chapter. Scientists identified mitochondrial and Y-chromosome haplogroups common among Native Americans and compared them to Asian haplogroups. Based on the idea of molecular clock, the mutations that separated Native Americans from Asians were used to calculate the evolutionary distance between these groups.[3] Mutation rates are, however, always estimates, and it is impossible to pin down the exact timing of a particular evolutionary event (in this case, the divergence of Asian and North American mitochondrial and Y-chromosome lineages).

For these reasons, scientists were eager to use DNA from Paleo-Indian human remains, as knowledge gained through aDNA would help circumvent the need to extrapolate a hypothetical past from contemporary DNA. As suggested above, aDNA was seen as providing empirical evidence of human evolutionary past as opposed to theoretical models based on modern samples—a framing that erases the fact that aDNA analysis, like population genetics in general, also relies on mathematical and statistical models. Ancient DNA was also seen as providing temporal depth, and thus a special vantage point to the passing of time that would flesh out the complexities of prehistoric migrations not preserved in the DNA of modern populations. Ancient human remains were, however, few and usually poorly preserved: the best known ancient remains included the two 13,000-year-old human femura (thigh bones) discovered in California in 1959–1960 and known as Arlington Springs Man, and the 10,000-year-old nearly complete skeleton found in Idaho in 1989 and known as Buhl Woman. This scarcity of ancient human remains partly explains why the 1996 discovery of an apparently racially ambiguous 9000-year-old skeleton near Kennewick in Washington State raised such high hopes of finding new answers—potentially using genetic analysis of ancient DNA—to questions about American prehistory.

Another reason for the affectively charged responses that the Kennewick remains raised lay in the complicated ethical and cultural questions surrounding the use of Paleo-Indian remains for scientific study. One such question concerned the use of indigenous biological material—genes, bones, health records—by white Western scientists for purposes not agreed on by indigenous groups themselves. This issue had haunted the Human Genome Diversity Project, which was initiated in 1991 to archive the evolution of human genetic diversity through DNA collected from

indigenous populations (Reardon 2005). It also underlay the way in which the DNA collected from the Havasupai tribe by Arizona State University in the early 1990s was circulated among research labs studying issues not related to the original project for which the DNA was collected (Reardon and TallBear 2012). Such use of indigenous samples reflected the assumption that indigenous people's bodies should serve the larger community—even when those individuals or their families have not consented (Reardon and TallBear 2012; Kowal et al. 2013; Kowal 2013).[4] Another question involved the long history of Western practice of including indigenous artifacts and ancient human remains in Western museum collections and exhibitions without consulting indigenous communities. In the 1990s, American museums still included hundreds of Native American artifacts or bones, although the significance of repatriation—the return of such culturally important objects to the communities associated with them—had been recognized by many museums and policy makers (Thomas 2000). Yet prehistoric human remains were often seen as too valuable for science to be simply handed to a local indigenous group for reburial.[5]

Finally, the use of ancient human remains to address the evolution of human diversity in North America was seen as suspicious by many because it seemed to give a stamp of scientific approval to old arguments about racial differences. While scientists had been keen to suggest that the population genetic understanding of human differences as gradual genetic variation in fact challenged distinct racial categories (e.g. Cavalli-Sforza 2000; Gould 1996), the concept of population appeared to carry much of the old problematic of race: the need to draw boundaries between populations and conceptualize them in biological terms (Hinterberger 2012; Reardon 2008). For example, in order to study the composition of modern populations, scientists need to connect individuals to specific populations, a task that involves methodological choices that often run against indigenous people's own conceptions of what constitutes belonging, membership, and recognizable ties (TallBear 2013; Reardon 2008).

When the Kennewick remains entered public consciousness in 1996, they became an object of a political struggle about the American national narrative, national versus communal modes of belonging, the nature of racial categories, the ownership of human bodily material, and the role of

new scientific technologies such as aDNA analysis in resolving these questions. As my analysis of the debate will demonstrate, these issues are all implicated in questions of temporality and knowledge: Who owns the past? Who gets to define the connection between the past and the present? And more specifically, who may decide whether prehistoric events emerge as part of—or outside of—national or ethnic trajectories of belonging? What makes the Kennewick controversy a particularly interesting case is that it illustrates both the larger conceptual challenges posed by the evolutionary framework for accounts of both national and communal roots, and the intricate politics of ethnic difference that underlies narratives of American origins.

The Kennewick Controversy

In July 1996, two college students watching a hydroplane race near Kennewick, Washington, stumbled upon a skull on the banks of the Columbia River. They contacted the police, who discovered more bones along the shore, presumably washed out of the bank during the flooding of the river earlier that year. The coroner called a local forensic anthropologist, James Chatters, who had previously examined bones for the coroner's office. Based on the shape of the skull, Chatters tentatively identified the remains as those of a Caucasoid male, and would have considered them as belonging to a late nineteenth-century settler but for one fact: there was a cascade point, the type of spear point used by Paleo-Indians, embedded in the pelvis. Chatters sent a bone fragment to the University of California at Riverside for radiocarbon dating, which determined it to be approximately 9300 years old.

The Kennewick remains' racial ambivalence was more than a matter of scientific curiosity. The 1990 Native American Graves Protection and Repatriation Act (NAGPRA) determined that any human remains found on federal land that could be associated with a current Native American tribe should be returned to that tribe.[6] Since the particular section of the Columbia River was under the jurisdiction of the US Army Corps of Engineers, local Native American groups could request repatriation. As the great age of the fossil made it to the press, the Confederated Tribes of

the Umatilla Indian Reservation, together with four other Native American groups, filed a request for immediate repatriation of the remains. Eight scientists filed a suit to challenge the repatriation, arguing that the remains were so old that they could not be affiliated with any tribe—and even if there was a link, it could be determined only through a scientific study of the bones. To complicate things further, other parties joined the controversy. Responding to the initial Caucasoid classification, a Californian neo-Norse pagan cult called the Asatru Folk Assembly filed their own suit, arguing that Kennewick Man was their ancestor. In 2001, after the Kennewick remains became linked with Polynesia and the Ainu of Japan, a man of Polynesian descent, J. P. Siofele, also filed a motion to claim the remains. These events demonstrate that ancient human remains were widely seen as playing a pivotal role in establishing a point of origins for ethnic, cultural, or ideological communities. Crucially, this interest in the remains did not take place simply through a dichotomy of science versus nonscientific communal history. As the case of the Asatru demonstrates, science could be invoked opportunistically in support of the racist pseudo-mythology of a nonscientific community and their claims to prehistoric ancestry on the North American continent.

The lawsuit filed by the scientists, *Bonnichsen et al. v. United States*, took nearly eight years to conclude. In 1998, the Kennewick remains were placed under the supervision of the Department of the Interior (DOI) and moved to the Burke Museum in Seattle, where no one was allowed to view them. In 1999–2000, the National Park Service conducted a series of tests (including an inconclusive DNA analysis) in order to determine whether the tribes were affiliated with the Kennewick remains as defined by NAGPRA.[7] In September 2000, after reviewing the results, Secretary of the Interior Bruce Babbitt sided with the tribes and ordered repatriation. The scientists filed an appeal, and in 2002, US Magistrate John Jelderks ruled that the tribes were not affiliated with the Kennewick remains in a way that would justify repatriation. Both the tribes and the DOI appealed. In February 2004, the Ninth US Circuit Court of Appeals upheld Jelderks's decision, granting the plaintiff scientists a permission to study the bones. The scientists were given limited and strictly scheduled access to the remains in 2005 and 2006. The results of these studies were finally published in 2014 in a scientific volume

edited by two of the plaintiffs, Douglas Owsley and Richard Jantz (Owsley and Jantz 2014). The volume included estimates of Kennewick Man's diet, physical injuries, and burial position. It also comprised craniological measurements, which found a resemblance to the Ainu in Japan, thus supporting earlier suggestions of shared ancestry with Japanese or Polynesian populations. However, the much awaited genetic analysis was still missing.

The Kennewick discovery was covered extensively in the local and national media. One of the most widely read early newspaper articles was Timothy Egan's "Tribe Stops Study of Bones That Challenge History," published in the *New York Times* in September 1996 (Egan 1996). Egan's piece clearly illustrates the cultural stakes involved in the Kennewick case, especially its implications for the idea of American national roots. Based on Chatters's initial Caucasoid hypothesis, Egan describes the ancient remains as "a riveting discovery" that "adds credence to theories that some early inhabitants of North America came from European stock." Egan also replaced Chatters's word "Caucasoid" with "Caucasian," an ethnic identification familiar from everyday politics of American multiculturalism. The idea of European ancestry gained further momentum when the first facial reconstruction of Kennewick Man by Chatters and sculptor Thomas McClelland was published in 1998 and became linked to the image of the British *Star Trek* actor Patrick Stewart. As Ann M. Kakaliouras (2008) observes, Kennewick Man has become a widely circulated popular figure on the Internet, appearing regularly especially on white supremacist websites, which claim that the true first Americans were white Europeans, not Native Americans. These suggestions of European ancestry participate in the ongoing cultural negotiations over ethnic diversity in contemporary America. At the same time, they also echo the above-described nineteenth-century Mound Builder myth, which insisted that Native Americans were preceded by an earlier European-linked civilization and thus not really native to the continent. These scenarios of European versus Native American historical primacy were reinforced by the common belief that contemporary ethnic categories—Native American, European, Asian—could accurately characterize past human diversity.[8]

Embedding national or communal origins in human evolution involves bridging the divide between history and prehistory. That is, it entails connecting prehistory—that which precedes written records and thus the reach of the archives—into the cultural systems of historical memory and the affective structures of the present. The Kennewick controversy sheds light on three aspects of such temporal negotiations. First, it casts the Native American idea of an oral historical continuum against the Euro-American view of prehistory as a mysterious terrain. For example, Rochanne Downs, a representative of the Great Basin Inter-Tribal NAGPRA Coalition, is quoted as saying: "We don't have a prehistory … We have one continuous history" (Kluger 2006). Similarly, the Umatilla officer Armand Minthorn refers to the tribes' "oral histories that go back 10,000 years" (Minthorn 2008, 42) and states that "[w]e already know our history" (Minthorn 2008, 43). Downs's and Minthorn's use of pronouns is telling: for them, this is a question of "we" and "our history," not US national or even American continental history.

This rhetoric of *us* versus *them* also underlies the plaintiffs' public statements. In Egan's (1996) article, one of the plaintiffs, Douglas Owsley, is quoted as saying: "If there is no further opportunity to examine these remains, we will be losing information that is important to every American." This rhetoric produces an imaginary national community of "every American" while insisting that knowledge provided by science will be relevant for Native Americans as well—even if they refuse to recognize this importance. Similarly, another plaintiff, Robson Bonnichsen, is quoted as stating: "This is a battle over who controls America's past … We have always used the term paleo-Indian to describe remains of this era. But this may be the wrong term. Maybe some of these guys were really just paleo-American." Such a rhetorical shift extends the imagined historical distance between Native Americans and Paleo-Indians to the extent that "paleo-American" emerges as the most accurate term to describe these early inhabitants of North America. As a result, Paleo-American heritage assumes temporal and thus epistemic primacy over Native American heritage. Interestingly, this suggests that the Kennewick controversy is not only about what counts as "indigenous" or "Native American" as stated in NAGPRA, but also what is "American," an ambiguous

word that invokes both continental pre-national history and a national body of people often imagined as white and European in historical accounts of the birth of the United States. While scientists tend to operate within the framework of continental prehistory, the legal parameters defined by NAGPRA and federal law foreground nationally framed interpretations of America and American population groups.

Second, the Kennewick controversy made explicit the belief that science may transgress the history/prehistory divide. This becomes evident in the common depiction of the remains as a historical document and of science as an act of deciphering their message, as when forensic anthropologist Hugh Berryman is quoted as saying: "The bone records its own history … This is like a rare book. We're reading a page at a time" (Smith 2005). Crucially, such a portrayal aligns science with progress, while casting indigenous tradition as an impediment to progress (Russell 2008, 78). Thus, the plaintiffs' lawyer, Alan Schneider, is quoted in the media as stating that "[s]cience can't proceed if scientists can't get access to new data" (Wilford 1999), and the *New York Times* cultural critic Edward Rothstein declares that repatriation decisions are motivated by "the desire not to fully explore but to fully appease" (Rothstein 2006). Many Native Americans have protested such claims by emphasizing that they oppose only the belief that science always provides the ultimate answer, not science as a mode of inquiry (e.g. Sampson 2008).

Third, these cultural negotiations over prehistoric knowledge are highly emotionally charged, as suggested by the recurring expressions of excitement, fascination, anger, and frustration by participants and commentators in the controversy. The emotional stakes are articulated particularly clearly in James Chatters's account of the controversy, *Ancient Encounters: Kennewick Man and the First Americans* (2002), in which he depicts his experiences as the first examiner of the bones and laments the fact that he was not allowed to complete his scientific investigation. The book is written in the language of deeply felt professional and personal duty: "the forensic anthropologist is the advocate for the dead, and as the individual who gathered this man's remains from the riverbank I feel a personal responsibility and attachment to him" (Chatters 2002, 269). This sense of emotional and moral accountability becomes associated

with the ethics of speaking and listening, as when Chatters states that "Kennewick Man had come to us from long ago, with many stories to tell of his life, his times, and his people" (Chatters 2002, 79). Conveniently vague yet emotionally loaded, the "us" that Chatters imagines have an obligation to listen and to learn. This rhetoric places Chatters's book at the heart of the heated debate over who counts as "us" and "they" in accounts of American prehistory.

Perhaps the most emotional aspect of Chatters's book is the emphasis placed on futurity. Dedicated to the "future generations of Americans, whose right to know the full story of their homeland's past was the motivation for this book," the book renders the past, present, and future as intimately connected. The sense of obligation that Chatters evokes is thus directed to a future:

> I felt a profound sense of loss. I had been given a gift from the past, an opportunity to learn from an ancient ancestor and to convey what he could tell me. I had not gotten the scientific corroboration needed to establish his validity as an early American. I had failed him. I had failed posterity. (Chatters 2002, 78)

This rhetoric of "having failed" both Kennewick Man and "posterity" indicates that national future is premised on the proper appreciation of the past. The obligation to future Americans, that is, is organized by a sense of longing for the past, which itself operates as a longing for the future. Significantly, such two-way yearning is ultimately nostalgic.

In the next chapter, I examine the affective dynamics of this prehistoric yearning and the understanding of two-way temporality that it relies on. The remainder of this chapter, however, focuses on the idea of prehistoric past as a cherished site where the roots of modern communities can be found. It shows how DNA retrieved (or imagined to be retrieved) from prehistoric human remains lends epistemic authority to visions of national, ethnic, and regional roots. At the same time, it explores how the prehistoric origins imagined through aDNA operate differently in national, ethnic, and regional modes of belonging.

Kennewick Man's DNA

During the legal battle over the Kennewick remains, the possibility of retrieving DNA from the remains was invoked several times. Many participants and commentators in the controversy suggested that DNA could establish whether Kennewick Man and the Native American tribes are affiliated. For example, Chatters maintains in *Ancient Encounters* that "the DNA would tell us whether he was modern European or American Indian" (Chatters 2002, 49). Likewise, the Asatru Folk Assembly's lawyer insisted in 1999: "Next step is a D.N.A. analysis. That's the bottom line that will determine everything" (Egan 1999). Crucially, this belief in DNA persisted even after the DOI scientists failed to analyze DNA during the trial due to the mineralization of the bones. A 2006 article in *Time* magazine muses that Kennewick Man's "bones have more secrets to tell" that could be deciphered if "DNA could be extracted and analyzed someday" (Lemonick and Dorfman 2006). And in a 2012 piece in *The Los Angeles Times*, Owsley is said to be "convinced a future team might have better luck extracting DNA from the skeleton, perhaps from its teeth" (Murphy 2012). This insistence on genetic analysis shows that DNA was seen as ultimate evidence that could determine categories, origins, and boundaries with precision that other modes of analysis presumably lack. In other words, it was seen as capable of settling the ambiguities suggested by cranial measurements, anatomical comparison, dietary science, or archeology. A silent witness residing inside the body, aDNA needed to be woken through careful analysis and persuaded to tell its first-hand account of the foundational events of the American past.

During the scientific study of the Kennewick remains in 2005–2006, it still seemed likely that Kennewick Man's DNA was simply too badly damaged to ever provide meaningful scientific results—although this did not stop scientists from fantasizing about it, as we saw above. However, the situation changed with the introduction of new sequencing technologies in the second half of the decade. After the publication of DNA results from a series of prehistoric human remains since 2010, including the sequenced genome of "Anzick-1," a 12,000-year-old Paleo-Indian male infant in Montana, it was no longer surprising when, in 2015, researchers at the University of Copenhagen announced in the

journal *Nature* that they had successfully sequenced Kennewick Man's mitochondrial and nuclear genomes (Rasmussen et al. 2015).

Intriguingly, the genetic analysis contradicted earlier interpretations of craniometric similarities between Kennewick Man and the Ainu and the Polynesians, and thus challenged the view that Kennewick Man represented an earlier wave of immigration from Asia to America that predated the one from which Native Americans originated. Comparing Kennewick Man's DNA with other Paleo-Indian remains (the recently sequenced "Anzick-1" genome), modern Native Americans (including the Colville, one of the tribes requesting repatriation, and the only ones who agreed to genetic testing), and several world populations, Morten Rasmussen and colleagues discovered that "the autosomal DNA, mitochondrial DNA and Y chromosome data all consistently show that Kennewick Man is directly related to contemporary Native Americans, and thus show genetic continuity within the Americas over at least the past 8,000 years" (Rasmussen et al. 2015, 458). They conclude that either "(1) the Colville individuals are direct descendants of the population to which Kennewick man belonged, but subsequently received some relatively minor gene flow from other American populations within the last ~8,500 years, in agreement with our findings above; (2) the Colville individuals descend from a population that ~8,500 years was slightly diverged from the population which Kennewick Man belonged or (3) a combination of both" (Rasmussen et al. 2015, 456–457). As to the craniometric similarities between Kennewick Man and the Ainu and the Polynesians, the researchers conclude that "Kennewick Man's pattern of craniometric affinity falls well within the range of affinity patterns evaluated for individual Native Americans" (Rasmussen et al. 2015, 458). Thus, the most publicly highlighted and visualized aspect of Kennewick Man's physique and a central focus of the debate about his racial classification—his facial features—was returned within the parameters of "normal" Native American body.

Rasmussen and colleagues' *Nature* article and its public reception reinforced the assumption that genetic analysis provided a conclusive, epistemically superior account of the prehistory of human populations. For example, a *New York Times* article on the DNA analysis was titled "New DNA Results Show Kennewick Man Was Native American,", and the article itself announced that the "analysis clearly established that

Kennewick Man's DNA is Native American" (Zimmer 2015). Similarly, based on the Danish team's initial DNA results in January 2015, *The Seattle Times* reported that "the mystery of [Kennewick Man's] origins appears to be nearing resolution" (Doughton 2015). Indeed, the results were widely seen as finally providing local Native American tribes with a strong case for repatriation—stronger than the ones based on oral narratives, cultural artifacts, or archeological reconstructions. It is noteworthy, however, that NAGPRA understands affiliation as cultural as well as biological (evolutionary, reproductive descent). For this reason, it is pivotal to ask what kind of evidence genetic analysis of ancient DNA actually engenders. What does mitochondrial, Y-chromosome, or autosomal DNA tell us about the connection between prehistoric individuals and modern communities?

What the Danish study showed was that the Kennewick remains and local Native Americans (represented by the Colville) shared genetic material of multiple kinds—autosomal, mitochondrial, as well as Y-chromosome DNA. It indicates that there is a clear reproductive continuum between modern Native Americans and the population that Kennewick Man belonged to, and that this continuum is not limited to a specific mode of inheritance—such as exclusively maternal (mitochondrial) or exclusively paternal (Y-chromosome) markers—but is reflected in the overall composition of the mitochondrial and nuclear genomes. However, Kennewick Man's DNA does not engender knowledge on cultural affinities or communal belonging. As Kim TallBear (2013) argues, the idea of DNA as the ultimate proof of ethnic affiliation is problematic in many ways—even when a DNA analysis may support a Native American claim of prehistoric roots, as in the Kennewick case. First, it privileges genetic markers over an abundance of cultural, archaeological, and geographical evidence, which, in many cases, are much more important for the forms of belonging that people experience and live with. Indeed, the insistence on DNA often confuses cultural tradition with molecular lineage. Second, in the context of Native American communities, it replaces the historical concept of the Indian Nation with the idea of biological race, which erases the complex cultural and social systems through which affiliation and belonging operate in Native American communities (TallBear 2003).[9] This does not mean that genetics should not be used to argue for an evolutionary connection—in the case of Kennewick Man, the genetic connection between

the ancient remains and modern Native Americans is an important empirical find. It does mean, however, that we need to recognize the limits of what DNA can tell us about belonging. We need to understand how knowledges produced through DNA analysis not only erase cultural and social inheritance; they also trace specific patterns of genetic inheritance that depend on the analytical technique (mtDNA analysis, Y-chromosome analysis, autosomal DNA analysis), collection of data, as well as statistical models used in the study.

Finally, the analysis of Kennewick Man's DNA provided both conceptual challenges and appealing resources for attempts to narrate American national origins in evolutionary terms. Apart from connecting the Kennewick remains to modern Native Americans, the genetic analysis also suggested "additional complexity in the population history" of Native Americans in North America: while the Kennewick remains were closely related to the Colville, they were more distantly related to the Anzick-1 Child, pointing to "the presence of an additional Northern lineage that diverged from the common ancestral population of Anzick-1 and Southern Native Americans"—this lineage "would include both Colville and other tribes of the Pacific Northwest" (Rasmussen et al. 2015, 456). This discovery rendered American prehistory affectively ambivalent. On the one hand, it embedded American origins in heterogeneity and multiplicity rather than singularity. It also discredited the idea of "Paleo-American" (as opposed to Paleo-Indian) population that had suggested that Kennewick Man was more closely related to prehistoric Asia than to Native American tribes. Instead, the genetic study rendered American roots explicitly Native American, as modern Native Americans were the only ones in whose cells American prehistory still lived. At the same time, the complexity of prehistoric genetic ties identified in the 2015 study did not support the idea of distinct, evolutionary rooted ethnic communities either.

On the other hand, the genetic continuum between Kennewick Man and the Colville helped to build a sense of forward movement, of tangible historical connection. This released the North American continent from a sense of timelessness, an absence of history. The Kennewick DNA embedded American prehistory in the forward-looking dynamic of genetic evolution, thereby producing an affectively appealing temporal trajectory between past, modern, and future American communities.

Furthermore, it shored up the epistemic role of the population genetic conjoiner of ancient and modern DNA as key to understanding how modern people belong to the diverse, evolving world. While this imagined conjoiner enacted belonging variedly as nationally, ethnically, or continentally framed trajectories in different stages of the Kennewick controversy, the assumption that genetic trajectories should be seen as primary to other forms of belonging never faltered.

Cheddar Man as a Historical Object

I shall turn now to another case of ancient human DNA, this time in the United Kingdom, which sheds further light on how the conjoiner of modern and ancient DNA enacts multiple modes of belonging. "Cheddar Man" is the name used for the human skeleton discovered in Gough's Cave near Cheddar in Somerset in 1903. Like the Kennewick remains, the Cheddar remains are approximately 9000 years old, and compared to most human remains, they are remarkably well preserved: Cheddar Man is the oldest complete human skeleton found in the United Kingdom. Unlike the Kennewick remains, Cheddar Man's bones did not invoke cultural or political controversy over ownership or the right to determine prehistoric origins. The Cheddar remains did, however, provide a widely welcomed addition to the project of establishing roots of the British people. Upon its discovery in 1903, the Cheddar skeleton was framed as the "earliest Englishman"—the same title given to the Piltdown hoax only a decade later—and was assigned wishful but unsubstantiated estimates of 40,000–80,000 years of antiquity (Stringer 2006, 137). As suggested at the beginning of this chapter, the need to find truly "English" human fossils arose partly from the competitive nationalist framework which pitted the remarkable prehistoric finds made in France and Germany against the absence of equivalent fossils on British soil. The perceived urgency to document "British" prehistory was also reinforced by the long history of Celtic, Roman, Saxon, Viking, and Norman population of Britain. Prehistoric human fossils, then, were seen as the desired antidote to the vagueness and "un-Britishness" of British history.

The Cheddar remains might have remained juts one human fossil among many if it wasn't for the mtDNA analysis conducted on the remains in 1997. This event rendered Cheddar Man the focus of a reinvigorated public debate about the connection between early inhabitants of Britain and its modern citizens. The emphasis placed on DNA as ultimate evidence of the roots of the British people reflected the imagined role of DNA in the Kennewick controversy taking place at the same time at the other side of the Atlantic. Yet the two invocations of aDNA differed significantly in how they structured the debate about roots. While retrieving and analyzing DNA was portrayed as the ultimate goal and final solution of the Kennewick inquiry, in the Cheddar case the jubilantly announced completion of the DNA analysis triggered a public debate about British roots and largely directed its course.

Another important difference between the Kennewick and Cheddar cases is the forms of belonging they invoked and refashioned. The Kennewick debate was fueled by tensions between three forms of belonging. The first was national belonging, which was understood as referring to the United States as a coherent cultural and historical entity rather than, for example, to the idea of Indian Nation. The second was belonging as continental, as an evolutionary continuum governing all of American prehistory, including Canada and South America. The third was ethnic and racialized belonging, which was understood, on the one hand, as Euro-American, and, on the other hand, as Native American. The Cheddar case, by contrast, enacted slightly different forms of belonging. First, the Cheddar remains became embedded in discourses of national belonging, that is, the evolutionary roots of modern Britain—or, in some accounts, one of its constituent nations, England. Second, this national framework became juxtaposed with regional belonging, the idea of the people of Cheddar as the true descendants of the prehistoric populations on the Isles. Third, these modes of belonging became entangled in discourses of personal belonging, as the closest contemporary descendant of Cheddar Man identified through DNA analysis was portrayed as having a personal family connection to Cheddar Man. These tensions between national, regional, and personal belonging in discourses surrounding Cheddar Man's DNA elucidate the cultural complexities of imagining origins through ancient DNA.

The analysis of Cheddar Man's mtDNA was conducted by Oxford University geneticist Bryan Sykes and colleagues as part of a West Country archeology television program called *Once Upon a Time in the West*. As it was still early days in aDNA research, the analysis relied solely on a limited set of mitochondrial markers. The idea was to compare mtDNA retrieved from Cheddar Man's molar with mtDNA collected from 20 students and teachers at a local school. The program culminated at a final get-together where the results of the comparison of aDNA and modern mtDNA samples were announced. As most of the samples were collected from underage teenagers, the program ended up highlighting the genetic connection between the DNA sample given by history teacher Adrian Targett and the one retrieved from Cheddar Man. Separated by one mitochondrial mutation, Cheddar Man and Adrian Targett were announced to belong to the same mitochondrial haplogroup known as U5. As mtDNA is inherited maternally, the connection identified between Targett and Cheddar Man could not be strictly direct. More likely, the results suggested that they shared a common maternal ancestor somewhere in the distant past. Furthermore, as U5 is a common haplogroup shared by about 10 % of Europeans, it is likely that wider sampling within the community would have generated a number of similar matches. Recently, some have also raised the possibility that mtDNA collected from the Cheddar bones may have been modern DNA resulting from contamination, the extent of which was not yet fully understood in 1997 (e.g. Bandelt et al. 2008).

Although the television program was intended for a regional audience, the results of the DNA tests generated nationwide and even international media reports, for example, in the United States. The ensuing media coverage portrayed DNA as the undisputable witness to the past and downplayed the scientific understanding that mtDNA represented only a small portion of genetic inheritance, and thus a very specific vantage point to human evolutionary past. It also erased the role of mathematical and statistical models in the production of knowledge about genetic relatedness. Encouraged by the framing of the television program, many journalists focused on the connection between Cheddar Man and Targett, thereby rendering genetic ties personal and singular. These highlighted connections became deeply entangled in affective investments and ideas of gendered difference.

Competing Forms of Genetic Belonging

The results of the DNA analysis became embedded in several culturally familiar narrative frameworks in the media.[10] Tabloids in particular framed the results within a humorous discourse of caveman masculinity resonating with popular culture. For example, *The Mirror* titled a piece on the DNA test with a Flintstones inspired wording "Yaba daba doo! Genes Prove Teacher's Old Man's a Caveman" (Dunn 1997), and entertained its readers with descriptions such as: "Adrian Targett does not seem the sort to strap a loin cloth and go out clubbing girls" (*The Mirror* 1997). Other papers also used humor, but in a less blatant manner.

The news were also framed within narratives of technological development. This involved both fears and fantasies of the possibilities of using aDNA. On the one hand, several pieces invoked Dolly, the sheep cloned in 1996, as a context within which the Cheddar case was set (e.g. Vrazo 1997; CBS News 1997). This involved invoking and subsequently rejecting the idea of cloning Cheddar Man, as when the Glasgow paper *Herald* wrote that the scientists "are no closer to bringing a Jurassic Park-style recreation to reality" (*The Herald* 1997; see also *The Scotsman* 1997). The texts calmed their readers' assumed anxieties by emphasizing that there were no intentions to clone the ancient ancestor, nor was it technically feasible. On the other hand, several newspapers invoked the possibility of evermore detailed analytical techniques that could trace Cheddar Man's eye and hair color and genetic diseases (e.g. *The Scotsman* 1997). As we know now, there kinds of techniques began to materialize with high-throughput sequencing technologies around 2010, when, for example, the physical appearance of the 4000-year-old individual from Greenland mentioned earlier in this chapter (Rasmussen et al. 2010) was investigated on the basis of autosomal DNA retrieved from hair preserved in permafrost. This is, of course, typical of the media responses to scientific technologies: as many have observed, and as I argued in the chapter on Mitochondrial Eve, technologies do not appear in a cultural vacuum but take shape within a larger cultural politics of emotion and temporality, including affectively charged expectations of what technologies can, and what they should do.

The specific role of analytical techniques in the production of knowledge was often downplayed in the media coverage. For example, several

media accounts referred simply to DNA rather than mtDNA, thereby omitting the fact that the genetic analysis engendered knowledge only about strictly maternal inheritance (e.g. *CBS News* 1997; *Scottish Daily Record* 1997; *NBC News* 1997; *ABC News* 1997). Accordingly, Targett was misleadingly portrayed as "a direct descendant" of Cheddar Man and their relationship as "the oldest direct genetic link between a modern and ancient human" (Vrazo 1997), even though this was impossible as mtDNA is inherited maternally: rather than directly linked, the two men shared a female relative somewhere in the past. There were also references to a "blood tie" (*The Toronto Star* 1997), a nonscientific concept carrying wide cultural resonance well beyond the parameters of genetic inheritance. Media reports also emphasized the decisive nature of the tests, as when *The Austin American-Statesman* wrote that "the DNA had conclusively shown Targett to be a relative of Cheddar's cave man" (Montalbano 1997). On the other hand, some texts acknowledged that had the scientists sampled a larger group, they would have likely found a number of equally close matches (e.g. Hawkes 1997; Vrazo 1997).

As the case of Mitochondrial Eve suggested, evolutionary descent is often entangled with familial discourse, which can be used to multiple political ends. This is also the case with the media coverage of Cheddar Man. While familial language often emphasized global, species belonging in the reporting on Mitochondrial Eve, in the Cheddar Man coverage it supports primarily the idea of belonging as personal—that is, it is literally seen as a matter of the family. Familial language recurs in a large number of media texts on the genetic connection between Adrian Targett and Cheddar Man. For example, Cheddar Man was referred to as "a long-lost relative" in *The Scotsman* (*The Scotsman* 1997) and a "caveman in the family" in the *Scottish Daily Record* (*Daily Record* 1997); Targett was portrayed as Cheddar Man's "living relative" in the Scottish paper *The Herald* (*The Herald* 1997); the two were seen as "close relatives" in *The Guardian* (Mihill 1997); and the cave was described as "the home of a close relative" in *The Independent* (Arthur 1997). Similarly, modern family life was cast as a mere variant of Mesolithic arrangements, as when *The Independent* described the Targetts as "a tribe who may not be adventurous but are certainly constant," a scientifically problematic statement as mtDNA,

unlike most surnames, is inherited maternally (Nuthall 1997). This kind of familial language made the results of the DNA test appear as reinforcing the importance of personal belonging to the evolutionary past.

This significance of personal belonging was reinforced by the recurrent invocations of emotion in the media responses. The initial coverage focused on Targett's reaction to the news, a theme that was repeated in a large number of texts. Targett was described as being "startled" (*The Toronto Star* 1997) and "stunned" (*Sunday Mail* 1997), and he was quoted as saying that he felt "overwhelmed, a bit surprised" (*The Toronto Star* 1997; *The Record* 1997) and that "It is very strange news to receive—I'm not sure how I feel at the moment" (Arthur 1997; see also Hawkes 1997). Targett is described as "coming to terms" with his newly established roots (Mihill 1997). The very assumption that Targett should have a strong affective response is suggestive that roots are deeply entangled with ideas of transformative experience and a sense of belonging and identity. It also suggests that roots are enacted through mobilization of emotions.

The discourse of personal, familial belonging was in contrast with the discourse of national identity that also arose in the media coverage. The connection between Targett and Cheddar Man was portrayed as releasing national history from the culturally unsatisfactory idea of British people as descendants of Roman, Saxon, Viking, and Norman occupiers, and thus as representing a mixture of "foreign" inheritance. In the media coverage, the test results were framed as establishing a much older lineage that rooted Britishness in a prehistoric landscape on British soil. *The Times* reported that the leading scientist, Bryan Sykes, believes that the genetic discovery provides "further evidence that the population of Britain is descended from the relatively few hunter-gatherers who lived 9,000 years ago" (Hawkes 1997), a framing repeated in *The Scotsman* (*The Scotsman* 1997). Similarly, *The Philadelphia Inquirer* saw the genetic evidence as providing "a new vision about Britain's ancient past," and, accordingly, portrayed Cheddar Man as "a Mesolithic-period Briton" (Vrazo 1997). Some reports combined narratives of national and personal roots, as when *NBC News* depicts Targett as "more English than England's royal family—the only one in the country with a prehistoric

pedigree" (NBC News 1997). All in all, these invocations of prehistoric national roots operate with a number of problematic concepts: they project modern national concepts (Britain, Briton) on the prehistoric past while muddling the politically charged distinctions between concepts such as Britain and England. They also reinforce the assumption that nation and its people are meaningful entities of genetic analysis.

There also emerged a third discourse of belonging in the media coverage: that of regional roots. A large number of news reports highlighted the fact that Targett lived only half a mile from the cave where the Cheddar remains were discovered and that his relatives had also stayed in the area (e.g. Montalbano 1997; ABC News 1997). This framing may have been popular because it fit the easily recognizable image of British country life as slow, local, and (to the outsider) charmingly eccentric. Crucially, however, this idea of prehistoric regional belonging was in tension with the discourse of prehistoric national roots. In many media reports, it appeared as if the truly ancient people were not the British nor the English but the people of Somerset or even the inhabitants of the village of Cheddar, a framing that was particularly prominent after the reconstruction of Cheddar Man's facial features was published in 1998, as we will see in the next section.

While the personal, national, and regional forms of belonging did not coexist without friction, they also supported one another in crucial ways. The way in which the three forms of belonging emerged as structurally parallel in the media coverage of the DNA analysis produced a highly affective temporal trajectory. Placed together, the three modes of prehistoric belonging reinforced the idea of belonging as an evolutionary, molecularly rooted phenomenon. Furthermore, the three discursive frameworks invested the idea of prehistoric belonging with different meanings, thus rendering belonging inherently contradictory. Yet it is precisely this multiplicity of meaning that gave the prehistorically embedded evolutionary trajectory wide cultural resonance. In this discursive multiplicity, then, resides both the affective appeal of the idea of belonging as prehistorically rooted, as well as the means of questioning its coherence and thus its cultural authority and persistence.

The Affective Rhetoric of Class and Masculinity

In the popular discourses surrounding Cheddar Man's DNA, affective investments were not only attributed to Adrian Targett's relationship to ancient human remains. Those remains were also imagined as affectively charged. Bryan Sykes, the geneticist who designed and conducted the DNA analysis on Cheddar Man's molar, describes his feelings toward the remains in the following way in his book *The Seven Daughters of Eve*:

> I don't find it particularly easy to relate a skull to a living person but, as I looked at the pieces displayed on the desk, I began to imagine the flesh and the skin of the head building up on the reconstructed skull. As I write this it sounds distinctly macabre, but at the time it wasn't in the least. In my imagination, these were no longer just lifeless fragments of bone but a real person. I had no clear impression of what he looked like—no idea whether he had black or fair hair, brown eyes or blue—but I did have a very strong feeling that this was a person. Strange, remote, from a far-off time, but a person none the less. What stories he could tell about his life, his family. (Sykes 2001, 176)

The emotional investments of this passage resemble strikingly those in James Chatters's depiction of the Kennewick remains in *Ancient Encounters*, quoted earlier in this chapter. While the language of bitterness characteristic of Chatters's text is absent here, Sykes, like Chatters, invokes an emotionally charged moment preceding a closer analysis—in Sykes's case mtDNA analysis—filled with anticipation about secrets hidden in the bones that the scientist-narrator might discover. As with Chatters's text, Sykes's description turns a scientific object—a reconstructed skeleton—into an embodied human being with lived experiences of family and communal life.

This idea of Cheddar Man's remains as embodying unique personhood was invoked and reinforced in the debate that surrounded the announcement in March 1998 that scientists had reconstructed his facial features. During the year following the DNA analysis, scientists at Manchester University used forensic techniques employed in the reconstruction of

murder victims' appearance in criminal investigation to re-create the looks of Cheddar Man. After the completed reconstruction was announced, the media reported widely that Cheddar Man had suffered several blows on the head, one of which had dislodged a bone splinter and thus caused an abscess between his eyes, which eventually led to his death at around the age of 40. The director of the study, Robert Stoddard of Manchester University, is quoted in several reports as commenting on Cheddar Man's health: "He was not a very comfortable and happy chap during his lifetime. I think he had a nasty headache quite a lot of the time" (White 1998a; see also Western Daily Press 1998a; Connor 1998). Remarks about Cheddar Man's appearance were also widely circulated in the media. For example, one of the leading British papers *The Times* reported that on the basis of the reconstruction, Cheddar Man appears to have had a "disfigured face" with "a twisted boxer's nose, a lopsided palate and scar tissue" and a generally "pugnacious appearance" (Jenkins 1998). Several papers described Cheddar Man's nose as "blobby" (Connor 1998; White 1998a; *Western Daily Press* 1998a), and at least one reported that Cheddar Man "probably suffered from irregular growth of the face during childhood" (Connor 1998).

These descriptions of the reconstruction of Cheddar Man's face raised affectively charged responses, which British newspapers were quick to invoke and relish. Clearly sensing this affective potential, the *Bristol Evening Post* interviewed Adrian Targett and quoted him saying that "There isn't much family resemblance after 9,000 years, I'm happy to say" and reported his wife Catherine responding: "Nobody could say Adrian has a blobby nose or a lopsided head. He has a nice nose" (White 1998b). The most important cause for emotional uproar, however, was Stoddard's statement that on the basis of the facial reconstruction, Cheddar Man probably "looked pretty much like any modern inhabitant of a Somerset pub." This quote was circulated widely in the media (e.g. Connor 1998; *The Mirror* 1998; *Western Daily Press* 1998a, b; White 1998a, b), and, as was to be expected, journalists—especially those working for tabloids—contacted pub owners in Somerset to hear their responses to Stoddard's unfortunate words. In a piece titled "Caveman Turns Ugly: Cheddar Man Recreation Compared to Somerset Drinkers," one of the major tabloids *The Mirror* reported that "Pub locals were in ugly mood yesterday

after a scientist compared their looks with a battered caveman," and included quotes from local pub owners saying that "Far from being ugly, my customers look normal" or "Our regulars are a fine-looking bunch" (*The Mirror* 1998). The *Bristol Evening Post* included quotes from the same pub owners, who stated that "Far from being ugly bumpkins, my regulars are mostly pretty sharp businessmen—and quite normal looking. I think they will be rather offended," and "This scientist has got some cheek. Our regulars are a fine-looking bunch of modern working men" (White 1998b). Invoking similar language of communal emotional upset, the *Western Daily Press* titled their piece humorously as "Noses Out of Joint" (*Western Daily Press* 1998b). How much of this emotional outrage was real and how much of it was invented by the media is difficult to say in retrospect, but the reporting certainly tapped into a very familiar cultural narrative that cast the city against the country, and the upper and middle classes against the working classes. Interestingly, this framing was in stark contrast with some suggestions made in reports about the DNA analysis a year before, as when *The Independent* quoted archeologist Dr. Larry Barham saying about Cheddar Man: "You could put a suit on him and he wouldn't look out of place in an office" (Arthur 1997).

I am interested in these tendencies and shifts in the media coverage of Cheddar Man because they point to how categories of difference interplay with ideas of evolutionary origins and belonging. I would suggest that through the facial reconstruction and its media coverage, Cheddar Man emerged as embodying several intersecting differences. First, the perceived clash between city and country was constructed through ideas of masculinity. In the 1997 media coverage of the DNA analysis, masculinity already played a key role, as the texts played with the ambiguity as to whether Adrian Targett had a little bit of prehistoric masculinity residing in him, or whether Targett represented modern masculinity entirely distanced from prehistoric ways of life. This ambiguity was operationalized, for example, in accounts that noted that Targett did his fair share of housework (Lyall 1997; Mihill 1997; *The Mirror* 1997) while also highlighting his preference for eating his steaks rare (Hawkes 1997; Lyall 1997; Mihill 1997; Dunn 1997). In this way, the media played with easily recognizable cultural discourses about evolutionary origins as not only residing quietly inside us but also possibly directing our behavior

and preferences (Oikkonen 2013). In the news texts on the facial reconstruction, the male population of Somerset replaced Targett as the focus of assumptions about masculinity, thus rendering the question of modern versus prehistoric masculinity regional. This engendered an ambiguous representation, which, on the one hand, reinforced the idea that Somerset is the truly ancient site of prehistory in Britain and the inhabitants of Somerset in the unique position of being able to claim prehistoric ancestry. This representation supports the regional framework for belonging already established in the debate about the DNA results a year earlier. On the other hand, the representation locks Somerset in prehistory, suggesting, through the comparison of Cheddar Man's reconstructed face and Somerset pub customers, that these men—and by implication the whole of Somerset—represent the prehistoric past rather than the present. Crucially, the representation operationalizes assumed differences between the rural working classes, associated with the past and thus with lack of progress, and the busy life of cities associated with progress. This representation is then contested through the voices of local pub owners, who insist on the essentially modern sensibilities of Somerset men. That these invocations of masculinity are also about class is further reinforced through the framing, invoked both in the 1997 coverage of the DNA analysis and in the 1998 coverage of the facial reconstruction, that juxtaposes Targett's prehistoric roots (and later those of the people of Somerset) with the considerably shorter pedigrees of British royalty and aristocrats. This all suggests that masculinity and class intersect in ideas of how we belong to the prehistoric past, and how the past belongs to us—or some of us. It also highlights that competing accounts of evolutionary belonging as personal, national, or regional are negotiated through a complex set of intersecting differences.

The facial reconstruction of Cheddar Man, then, invoked a clearly different set of embodied differences than the facial reconstruction of the Kennewick remains. While both attempts to embody prehistoric ancestors—and implicitly prehistoric masculinity—triggered emotional responses, the former mobilized assumptions of class and regionalism while the latter tapped into cultural assumptions about race. This points to the flexibility and mutability of scientific knowledge in culture and society in the sense that the reconstructions were interpreted through

those narratives of belonging that were most prominent in the cultural contexts in which the remains were discovered and examined. Crucially, in both cases there were more than one prominent, culturally recognizable narrative—Euro-American (framed as all-American) and Native American in the Kennewick debate, and personal, regional, and national in the Cheddar case. This further underlines that evolutionary belonging as imagined through population genetics emerges through a complex set of evolutionary trajectories that are context dependent and mutually embedded. In the last two sections of this chapter, I will take a closer look at two aspects of these configurations of origins: the assumption that prehistoric origins reside inside us, and the assumption that genetic origins constitute an affective space.

Origins Inside Us

This chapter has argued that techniques and technologies of comparing ancient and modern DNA have reshaped ideas of belonging in important ways. They have produced a specific rewriting of temporality in which the past is no longer an inference based on mutations in modern DNA, as was the case with Mitochondrial Eve and Y-Chromosome Adam in the previous chapter. Instead, the past appears as rooted in the perceived materiality of prehistoric DNA. One result of the use of ancient DNA has been that the human evolutionary history appears as more complex than previously, as it includes also lineages present in ancient samples but absent in modern ones. Furthermore, the introduction of genome-wide techniques outlined an increasingly intricate web of connections between extinct populations, such as Neanderthals and Denisovans, as well as between past and modern populations, as in the eventual analysis of Kennewick Man's DNA and its relationship to past and present Native American groups.

The genetic comparison of aDNA and modern DNA is part of what Marianne Sommer (2006) calls the search for "history within," that is, scientists' long-standing attempt to discover human history by turning to the materiality of human bodies through paleontology, evolutionary theory, and population genetics. I would like to elaborate here briefly on the

specific configuration of roots that arises from the comparison of modern and ancient DNA. While it is true that metaphors portraying genetic material as an archive or museum were invoked in discourses surrounding the Human Genome Project and the Human Genome Diversity Project throughout the 1990s and early 2000s, such metaphors have attained special weight in the study of ancient DNA. With techniques connecting modern DNA samples to samples retrieved from ancient human remains, the body of the modern citizen has emerged as the true archive in the sense that it does not only point to current human composition or diversity, or serve as a basis of abstraction about the past, but is understood to carry origins in the materiality of its DNA sequences inherited from prehistoric human ancestors. Crucial here is the way in which the DNA retrieved from ancient human remains accrues a sense of concrete materiality, which is then translated into the materiality of modern DNA inside our bodies. This brings roots from the distant prehistoric past to our living, breathing, feeling bodies in the present. As a result, our connection to prehistory appears as highly intimate, affective, and always alive. This reconfiguration of roots is reinforced by a larger affective shift surrounding scientific technologies, as the successes of ancient DNA analysis during the past ten years have engendered new optimism about the possibility of tracing human evolutionary origins beyond abstract speculation.

The idea of evolutionary origins as living inside us informs a number of popular scientific accounts of belonging and roots in contemporary society. One illustrative example is Bryan Sykes's popular book *Blood of the Isles: Exploring the Genetic Roots of Our Tribal History* (2006), published in the United States as *Saxons, Vikings, and Celts: The Genetic Roots of Britain and Ireland*. As the shift between the titles for British and American audiences suggests, the book mobilized population genetics to tell two narratives of belonging: one about British and Irish ("our") "tribal history," which would divide the populations of Britain and Ireland into localized "tribes," and another one for American audiences highlighting the genetic story of two nations, Britain and Ireland. This shift between *regions* and *nations* is suggestive of the ways in which genetic belonging is always multiple and ultimately ambiguous. While Sykes's book utilized

aDNA only briefly in accounting the case of Cheddar Man, its portrayal of modern inhabitants of Britain and Ireland as living genetic archives arose largely from this scientific framework.

While framing his study as motivated by scientific interest, Sykes's book ends up glorifying the idea of prehistoric clans and ancestors. Anne-Marie Fortier (2011) has identified a similar thematic in the Channel 4 documentary *Face of Britain*, which, like Sykes's book, attempted to map British populations into ancestral groups on the basis of their genes. Fortier locates a nationalist and racist rhetoric in *Face of Britain*, which equates those whose families have resided within the nation for centuries as "indigenous" Britons presumably threatened by immigration and consequent multiculturalism, which are likely to wipe out "authentic" British genetic inheritance. Significantly, both Sykes's account and the one put forward in *Face of Britain* insist on the importance of purity of descent, whether for the sake science or for the preservation of national genetic inheritance. In both accounts, certain population groups emerge as more valuable sources of DNA than others. As a result, some people or groups appear as more ancient, more *purely* connected to the evolutionary past than other people or groups.

Evolutionary origins, then, appear to reside inside each of us, but in some of us they are assumed to be purer, less tainted by mixture, and thus more valuable for the scientist or the community. This is a central paradox of population genetics: we are all descended from the same unified origins and thus have equally ancient roots, yet some appear as if carrying a closer connection to the past than others. To put it slightly differently, evolutionary belonging, as constructed through population genetics, relies on a dynamic of differentiation. Differences recorded in people's DNA are both the primary source of evolutionary knowledge for population geneticists and the concrete materialization of processes of evolutionary change. Difference, that is, is the most important mechanism through which the connections between the past and the present are evaluated, imagined, and enacted. While difference is something we all embody, it does not become distributed equally in bodies. As the news coverage of the connection between Cheddar Man and Adrian Targett showed, the population genetic framework casts certain bodies as charac-

terized by *sameness*, a resemblance across time. In this configuration, difference as embodied in people's DNA is good, yet sameness (such as that between Targett and Cheddar Man, or between Kennewick Man and the Colville) is where true value lies. It is through sameness between modern and ancient DNA that the most tangible and affectively powerful trajectories between the present and the past are engendered. Crucially, this dynamic of differentiation is blurry in that the line between sameness and difference can be drawn differently depending on whether belonging is understood as personal, regional, ethnic, or national. I will return to this blurriness of population genetic communities in Chap. 5.

Affective Trajectories

Roots are commonly understood as evoking both cultural and personal emotions, and it is therefore no surprise that accounts of the genetic origins of populations are charged with widely resonant affective potential. The conjoiner of ancient and modern DNA in population genetics does, however, invest origins and the trajectories connecting us to them with specific kind of affective undertones. These undertones arise from the assumption that the use of aDNA renders evolutionary origins material and concrete rather than abstract and inferred. The ways in which the population genetic framework makes it possible to imagine our connection to the past as preserved in the most valued molecule in modern science and society gives affective primacy to genetic roots over other ways of conceptualizing origins. As I have argued throughout this and the previous chapter, this primacy of genetic materiality is illusionary in the sense that the study of ancient and modern DNA is dependent on mathematical and statistical models. Since molecular samples alone do not tell scientists anything, roots constructed through aDNA are always abstract rather than concrete. Yet, especially popular discourses surrounding aDNA typically insist on the idea of direct, unmediated access to the past. This insistence on tangible, unambiguous materiality operates as a rhetorical tool through which a wide range of cultural emotions about roots and relatedness can be invoked.

The shape of evolutionary connections produced through aDNA is also intimately tied to the use of specific technologies. As the different estimates of the connections between the Denisovan and the Neanderthal demonstrate, different analytical techniques and technologies may produce different trajectories of evolutionary descent. This shows that roots are not locatable in individual DNA sequences contrary to popular discourses surrounding the comparison of ancient and modern DNA. Rather, roots are enacted somewhere between individual modern DNA samples, aDNA samples, and existing databases of contemporary genetic diversity. Roots reside neither in the prehistoric bones nor in the cells of modern people, but are being constantly constructed and reconstructed through the development of new techniques of genetic analysis. Crucially, this ongoing population genetic project of constructing roots is made possible by the fact that most human DNA is not unique to any of us, but shared across space and time. Yet what emerges in the news coverage of Cheddar Man's DNA is a firm belief that Adrian Targett and Cheddar Man are connected materially through the indisputable fabric of DNA, and that this presumably unique connection is characterized by very special kind of emotional weight.

The technologically constructed nature of origins in aDNA studies (and population genetics more generally) is a key reason why evolutionary trajectories can be enacted in multiple ways. As the case of Mitochondrial Eve showed, the idea of evolutionary history as recorded in DNA resonates with mutually contradictory frameworks of belonging. The Kennewick and Cheddar cases indicate that the genetic study of ancient human remains can be incorporated into various narratives of belonging that enact origins in different, culturally recognizable ways. One narrative of belonging centers on personal belonging, as when the media interprets the molecular similarities between Adrian Targett's and Cheddar Man's mtDNA as a family connection, a matter of personal roots. Another narrative of belonging invokes ethnic or racial belonging. As the public controversy over the racial identification of the Kennewick remains showed, the very idea of ethnic or racial origins can also be mobilized in multiple ways, indicating Native American prehistoric primacy as well as Euro-American heritage. A third narrative

of belonging appeals to the long-standing tradition of telling the origins of the nation through prehistoric fossils. In the Kennewick case, this narrative resonated at times with the idea of Euro-Americans as a prehistoric racial group, and at times with the seemingly apolitical framework of all-American scientific and cultural interest. In the Cheddar case, national belonging took a different form, as it was not framed within internal politics of race or ethnicity, but rather became part of the larger project of establishing the evolutionary roots of Britain on British soil. This specific narrative of national belonging became then juxtaposed with regional belonging, the fourth narrative of belonging discussed above.

While these four narratives of belonging appeal to different ideas of what should determine our relationship to our social surroundings, they all invoke a similar set of cultural emotions ranging from pride, privilege, and celebration to envy, shame, and amusement. These emotions are not fixed, however, but can be appropriated and reworked to various ends. For example, pride and celebration can be located in the discourses of the antiquity of Native Americans or the people of Somerset, but they resonate differently in the context of the racial undertones of the Kennewick controversy and the less openly political juxtaposition of city and country in the Cheddar news reporting. Crucially, both invocations of pride and celebration become embedded in long and intricate histories of American and British cultural and societal dynamics, which set the parameters within which these emotions are interpreted and experienced. The invoked emotions also intersect with assumptions of differences such as class, gender, and race in multiple ways, as when pride in ancient origins becomes embedded in ideas of class and masculinity in the Cheddar media coverage. This affective multiplicity echoes closely the cultural travels of Mitochondrial Eve and Y-Chromosome Adam traced in the previous chapter. What has changed is the modes of genetic belonging that are being evoked and imagined: while the Mitochondrial Eve debate centered on the question of shared human ancestry, the Kennewick and Cheddar cases focus on increasingly localized relationships involving national, ethnic, regional, and personal forms of belonging to the evolving world.

This brings me to the final point of this chapter. The ways in which geneticized origins emerge as an affective space for imagining belonging also depend on the scope of evolutionary time that is being mobilized. While claims about Cheddar Man's mtDNA enabled multiple narratives of belonging, the point of origins in 9000 years in the past excluded imaginaries that would have highlighted belonging across human populations (or across species) by going "deeper" in the past—that is, it excluded the kinds of imaginaries that initially surrounded the figure of Mitochondrial Eve. Had scientists and TV producers explored the connection between Adrian Targett (or another modern person) and Neanderthal remains, the forms of belonging that would emerge would have been quite different from those mobilized in the Cheddar Man analysis and news coverage. To put it slightly differently, an ancient human DNA sequence is never simply a point of origins for modern communities or identities, but also a product of another point of origins still further in the evolutionary past.

Origins, then, are ambiguous and flexible in that they can be moved backward and forward in evolutionary time depending on the modes of belonging that are being enacted. In this sense, population genetic models of belonging are ultimately relational, constructed through temporal and spatial relations, as Amade M'charek (2005, 21–55) shows in her analysis of *population* as an adjustable analytical category in forensic genetics. Yet evolutionary distance does not determine the affective uses of population genetic origins. Rather, the precise age of aDNA samples intersects with cultural discourses of belonging so that certain forms of belonging—say, racialized and national belonging—may be more likely to emerge in certain contexts (such as US cultural politics) than others (such as the history of Britain).

This temporal dynamic of evolutionary belonging is the topic of the next chapter. Turning to fictional narrative and cultural and queer theory, I will explicate and theorize the ways in which the idea of evolutionary origins as affective space is connected to the present and the future. The chapter shows that the evolutionary trajectories of belonging that population genetics have engendered rely on an intricate temporal dynamic that could be called *evolutionary nostalgia*.

Notes

1. The idea of unmediated access is present in today's accounts as well. For example, Guido Brandt and colleagues portray aDNA studies as "providing direct genetic evidence" (Brandt et al. 2015, 73), and Luca Ermini and colleagues state that, thanks to aDNA studies, "one can now directly access our evolutionary past" (Ermini et al. 2015, 4).
2. For examples of different positions on prehistoric migrations from Asia to America, see Mandryk et al. (2001); Vasil'ev et al. (2002); Goebel et al. (2008); Erlandson and Braje (2011); Misarti et al. (2012).
3. For developments in the debate about the genetic roots of Native Americans between 2000 and 2010, see, for example, Eshleman et al. (2003); Starikovskaya et al. (2005); Kemp et al. (2007); Malhi et al. (2007); Tamm et al. (2007); Kitchen et al. (2008); Fagundes et al. (2008); Perego et al. (2009).
4. A similar attitude has also underwritten the use of African-American samples, for example the case of Henrietta Lacks mentioned in the previous chapter. See Priscilla Wald (2012) or Karla FC Holloway (2011, 1–24). The use of ethnically associated biolocal material in pharmaceutical industry, criminal investigation, and medically oriented genetic databases has also received wide criticism. See Jonathan Kahn (2010, 2013), Pamela Sakar (2010), or Sandra Soo-Jin Lee (2006).
5. These are, of course, not the only two options. Collaboration between scientists and indigenous communities has resulted in arrangements in which scientists may conduct certain tests as long as the remains are then given to the indigenous community (Tsosie 2012a, b; TallBear 2013, 177–204).
6. David Hurst Thomas (2008, 10–11) observes that with NAGPRA, "archaeologists had lost their monopoly on the deep American past. For the first time, Native American people were bona fide stakeholders in the national narrative, and they demanded to be heard."
7. The DOI scientists' reports and Babbitt's decision are available on the National Park Service website at http://www.nps.gov/archeology/kennewick/index.htm.
8. James D. Nason (2008) provides a critique of this assumption in the context of the trial.
9. See also TallBear's (2013) critique of the use of commercial genetic tests to resolve tribal affiliation.

10. Most of the media texts on Cheddar Man analyzed in the following sections were located through the LexisNexis database using "Cheddar Man" as a search term.

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4

Evolutionary Nostalgia and the Temporality of Belonging

In contemporary culture, DNA has emerged as a symbol of timelessness and immutability. DNA is frequently depicted as having endured throughout the dramatic cultural and social changes of the past millennia, and thus as being capable of transgressing time. These temporal underpinnings underlie, for example, evolutionary biologist Richard Dawkins's widely read popular book *River Out of Eden: A Darwinian View of Life* (1995). The central metaphor of the book is that of a river running through geological time. Dawkins writes: "The river of my title is a river of DNA, and it flows through time, not space. It is a river of information, not a river of bones and tissues: a river of abstract instructions for building bodies, not a river of solid bodies themselves. The information passes through bodies and affects them, but it is not affected by them on its way through" (Dawkins 1995, 5). Dawkins's portrayal builds on a juxtaposition between the immutability of DNA and the perceived short-lived nature of bones and tissues. This juxtaposition erases the fact that bones and tissues are a necessary source of DNA, and thus a precondition of genetic knowledge about the evolutionary past and the emergence of contemporary genetic diversity.

The idea of timeless and immutable DNA draws on the conception that genetic knowledge is pure and uncompromised, and thus unlike

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other phenomena in the natural world. Again, Dawkins's book provides an illustrative example. According to Dawkins, "[g]enes are pure information—information that can be encoded, recoded and decoded, without any degradation or change of meaning.… DNA characters are copied with an accuracy that rivals anything modern engineers can do. They are copied down the generations, with just enough occasional errors to introduce variety" (Dawkins 1995, 22). However, things are more complicated than the passage suggests. First, as we saw in the previous chapter, the evolutionary past captured in the presumably timeless DNA is relational: it arises from the choice of method and analytical technique as well as the availability and choice of material such as tissue and blood samples, cell lines, or reference sequences. That is, the choice of method and material *produces* patterns of difference and sameness through which the evolutionary past is enacted. Second, although DNA is, as Dawkins puts it, "digital information," DNA is not strictly immutable (Dawkins 1995, 22). As the debate about ancient DNA showed, DNA degrades in unfavorable conditions, constituting a major challenge in the study of human and animal remains. Also, while the average mutation rates can be calculated retrospectively, individual mutations may emerge at unpredictable moments and unanticipated molecular sites. Third, as I suggested in the previous chapter, the connection between the past and present captured in DNA is ontologically ambiguous. The ways in which the past and present emerge as connected may enact multiple forms of belonging, such as regional, ethnic, personal, or national belonging.

This chapter explores how temporality organizes population genetic knowledge and the forms of belonging that have emerged with it. While I start with the widely circulating idea of DNA as a historical archive or witness to the passing of time, my analysis complicates this portrayal. I suggest that population genetic knowledge is organized by a set of highly intricate, multidirectional temporal connections between the past, present, and future. In this temporal dynamic, neither past, present, nor future is single or uniform. Instead, there emerge multiple pasts and multiple presents, and, consequently, multiple futures. This temporal multiplicity draws on the metaphorical role of DNA as a tool that can connect us affectively to various constellations of roots and destinies. Such temporal multiplicity engenders tensions and ambiguities, which underlie and

organize the ways in which population genetics becomes a source imagining and enacting belonging.

The chapter explores a particular temporal arrangement, which I call *evolutionary nostalgia*. Evolutionary nostalgia is an affectively charged configuration of the connections between us, the past and the future that underlies a number of recent and contemporary narratives about evolutionary past. It resonates with, and is strengthened by, the idea of DNA as a molecular clock that records evolutionary history. I argue that evolutionary nostalgia reinforces a sense of longing for the past, which in turn operates as a way of imagining an alternative present and future. This two-way longing roots us in an evolutionary past while rendering that past the location of futurity. At the same time, the affective investments of evolutionary nostalgia function to domesticate the temporal ambiguities and the fluid dynamics of difference and sameness that characterize population genetic accounts of roots and belonging. However, the chapter also shows that despite the totalizing tendencies of evolutionary nostalgia, alternative temporal constellations and dynamics of difference reside as possibilities in the very idea of DNA as a means of belonging.

In what follows, I trace and analyze evolutionary nostalgia and population genetic temporality with the help of theoretical insights that have emerged from cultural studies of genetics, queer theorization of time, and the study of collective memory. Drawing on these fields of scholarship, I seek to explicate the complexities of time in population genetics, its relationship to larger questions of reproduction, kinship, and futurity, and the ways in which it evokes and shapes affective investments and cultural emotions. The first sections of the chapter tackle these questions. They are followed by a close reading of two works of fiction. The first of the texts, Kathleen O'Neal Gear and W. Michael Gear's popular prehistoric romantic novel *People of the Raven*, shows how evolutionary nostalgia operates as a means of imagining evolutionary history. The second text, Margaret Drabble's novel *The Peppered Moth*, complicates the smooth operation of evolutionary nostalgia by thematizing the multiplicity of temporalities and the entanglement of differences that underlie the two-directional working of evolutionary nostalgia. Both texts build on real-life debates about human evolutionary history: *People of the Raven* imagines the events surrounding the life and death of Kennewick Man,

and *The Peppered Moth* tells the story of three generations of mothers and daughters in the context of a mitochondrial analysis of ancient human remains very similar to the Cheddar case. Through my reading of *People of the Raven*, I show how evolutionary nostalgia domesticates differences through the creation of parallel presents and futures. I identify how evolutionary nostalgia connects the past, present, and future, and how the crafting of these connections rewrites different forms of belonging as if they were only one. That is, evolutionary nostalgia choreographs different forms of belonging into a seemingly coherent whole that supports a specific version of belonging. My reading of *The Peppered Moth* continues the discussion by turning the analytical focus to the unresolved tensions that remain despite the unifying affective work of evolutionary nostalgia. I suggest that Drabble's novel makes visible moments of temporal ambiguity and its connections to entangled differences such as gender, class, and race, and that such moments constitute cracks in the affective appeal of evolutionary nostalgia. The article concludes with a discussion of attempts to construct the genetic genealogies of Barack and Michelle Obama. Through the popular representation of the Obamas' DNA, I elaborate on how evolutionary nostalgia operates in society at the interface of genetic and cultural history as well as that of private and public history, and how DNA emerges as a tool of collective memory through which multiple forms of belonging unfold.

Temporality of Genes

Population genetics is organized by temporal investments that differ significantly from those of many other fields of genetics. Population geneticists are not interested in how DNA directs the building and functioning of bodies in the present or the future, but in the ability of DNA to tell us about our evolutionary past and the origins of current genetic diversity. In this sense, the temporal orientation of population genetics is toward the past. This orientation is reflected in the idea of *molecular clock* (e.g. Zuckerkandl and Pauling 1962; Margoliash 1963; Sarich and Wilson 1967; King and Wilson 1975) explored in connection to Mitochondrial Eve in Chap. 2. Molecular clock assumes that mutations in biomolecular material such as specific DNA sequences measure the evolutionary distance between species and populations. In the process, DNA emerges as

a metaphoric witness to the passing of time between moments in the past when species or populations diverged. While the idea of molecular clock has informed population genetic analysis of especially nonrecombining and noncoding DNA (found in mitochondria and a section of the Y chromosome) for several decades, the development of advanced sequencing technologies in the new millennium have complicated the picture. As the case of the 5000-year-old Greenland remains mentioned in the previous chapter suggested, population genetics is becoming increasingly interested in the coding nuclear DNA. This shift brings together noncoding DNA used as a past-oriented "molecular clock" and coding nuclear DNA as a key player in the production of physical characteristics such as susceptibility to specific illnesses. In this chapter, however, I focus primarily on how the idea of molecular clock configures temporality, as the logic of molecular clock plays a key role in cultural narratives of evolutionary origins and genetic belonging.

I want to begin by suggesting that the temporal investments of the molecular clock are more complicated than may first appear. Scholars studying the cultural aspects of genetics have explored especially the ways in which past and future emerge as mutually embedded in genetic knowledge. This temporal configuration arises, to a large extent, from the notion of DNA as digital knowledge—a kind of computer code—and thus as rewritable. Jay Clayton has used the concept *genome time* to refer to the distinct conception of time that emerges from this understanding of genetic knowledge. According to Clayton, in genome time "the present is made to contain every possible permutation of time as a suddenly legible system of signs" (Clayton 2002, 33), so that "[t]he past and future appear inscribed, as theoretical possibilities, within the mathematical space of the code" (Clayton 2002, 35). DNA is timeless in the sense that it can be rewritten, even if only in theory, in order to produce a different present and an alternative future. This temporal dynamic relies on a paradox: while genome time ascribes mutability to DNA (as a way to craft a new, alternative future), it also insists on the immutability and reliability of DNA as a historical record. Indeed, the capacity of DNA sequences to be rewritten relies on the assumed stability of genetic information.

The existence of parallel temporalities as virtual possibilities has foundational implication for the trajectories that emerge between past and

future. Drawing on Clayton's genome time, Priscilla Wald (2000) has explored how the future becomes embedded in the past in genetic discourse. According to Wald, "[i]mplicit in the mapping of the human genome is the possibility (often disclaimed) that geneticists will be able to alter their perspective of human fate, to transform time, in effect, such that the perspective on the future resembles our current perspective on the past" (Wald 2000, 698). Wald refers to this new understanding of time as that of future perfect, since it involves "the sense not only of being able to predict the expression of certain genes (simple future), but of being able to specify those predictions temporally and understand the conditions of gene expression in order to look forward as though looking back (future perfect)" (Wald 2000, 698–699). While both Clayton and Wald were writing at the time when the Human Genome Project was reaching its conclusion, their insights about the temporal ambivalence of genetic knowledge extend to population genetics as well. Indeed, Wald's analysis of the study that compared the spread of bubonic plague in medieval Europe to genetic resistance against HIV among contemporary racialized populations (discussed in the connection to Mitochondrial Eve in Chap. 2) shows that population genetics and its medical applications are informed by a conceptual and rhetorical collapse of the past, present, and future into one another.

This collapse is particularly central to the idea of cloning organisms from DNA samples. In terms of temporality, cloning could be described as a manipulation of DNA to rewrite the future. While the DNA manipulation may represent either the present (as in the act of cloning Dolly the sheep) or the past (as in fantasized accounts of the possibility of cloning from ancient DNA), it is especially in the idea of re-creating long-extinct species that the collapse of temporal zones is most clearly manifest. Building on Clayton's genome time, Stephanie Turner (2007) has interrogated the temporal investments of the cloning of ancient DNA. Analyzing "extinction narratives" that hype the perceived power of emerging cloning technologies, Turner writes: "In genome time, evolutionary histories, including extinction narratives, are revised, forestalling or even reversing absolute endpoints in the endless reproducibility of the DNA code. While the extinction of long-gone species remains an undeniable ending, the endless reproducibility of DNA renders all extinction

open-ended" (Turner 2007, 59). Preserved in a tooth or bone discovered in permafrost, the past becomes a source of rewriting the future. While the visions of cloning extinct species are largely incompatible with current cloning technologies, the very idea of rewinding time by cloning ancient DNA appears as logical and rational. This sense of logical necessity underlay some of the news reports about Cheddar Man's mitochondrial DNA (mtDNA) in the previous chapter. Crucially, the sense of logical necessity arises from the notion that DNA is an uncompromised digital record of the past.

DNA sequences are temporally invested also as scientific objects. In her analysis of the mitochondrial reference genome, Amade M'charek (2014) outlines how a DNA sequence enacts different temporalities in different scientific practices. M'charek draws on Michel Serres's understanding of *topological time*: instead of being linear, time is gathered and crumpled in objects, so that an object embodies multiple potential temporalities. M'charek shows how the mitochondrial reference genome "indexes and enacts its history" (2014, 29). Published in 1981, the original reference genome included three sources of genetic information derived from a placenta, the HeLa cell line (discussed in Chap. 2 of this book) and bovine mitochondrial DNA. However, these histories of making—especially in terms of the racial origins of DNA—were erased to construct a reference genome. Yet these histories unfold in unexpected ways as the reference genome is resequenced following developments in sequencing technologies, as well as studied to answer new kinds of research questions in adjacent fields such as medical genetics. M'charek emphasizes that "[f]olded objects are not political because of *what* is put into them, but because of *how* they are folded" (2014, 50; emphasis original). This draws attention to the practices of science. How objects are folded is often a matter of situated decisions that seek to solve practical methodological or technical challenges arising from the availability of genetic material or technological equipment. They also reflect institutionalized practices that are wider and run deeper than the work of an individual scientist.

This understanding of DNA sequences as *negotiated objects* constructed through material, technological, and epistemic conditions foregrounds several tensions that underlie genetic knowledge. As constructed objects,

reference sequences highlight the connection between abstraction and materiality. The purpose of a reference sequence is to serve as a point of comparison for other sequences analyzed later, that is, as a point of comparison through which the uniqueness of other sequences can be established. At the same time, a reference sequence is arrived at through the material details of specific samples and the technologies and techniques that study them. M'charek's analysis shows, however, that the situation is even more complicated: the mitochondrial reference genome remains scientifically meaningful only through a reanalysis of the original biological material and reevaluation of the accuracy and usefulness of the reference genome. This produces back-and-forth movement between abstraction and materiality. This movement shows the blurriness of the line between DNA as the unique property of an individual (DNA as difference) and DNA as shared inheritance (DNA as sameness). Depending on how the folded temporalities of the reference sequence unfold, various alternative constellations of difference and sameness emerge. The process of making differences and sameness through comparisons of DNA—the driving force of population genetics—thus emerges as entangled with folding and unfolding temporalities.

Furthermore, drawing on M'charek's analysis, I would also suggest that we need to pay attention to the different ways in which molecular objects of different size enact time. For example, a single nucleotide polymorphism (SNP) such as an ancestry informative marker (AIM), a longer DNA sequence, and a complete mitochondrial or nuclear genome embody different conceptions of how genes record history. They also carry different histories of their own making that are tied to the specific conditions in which each emerged as a meaningful scientific object. Due to these various folding and unfolding temporalities, different types of molecular objects are entangled with ideas of abstraction, uniqueness, or materiality in different ways. Whereas a single nucleotide appears as tightly rooted in the material processes within bodies, complete genomes are understood more easily to be objects constructed through scientific study. Yet single nucleotides, too, are products of past histories of scientific practice, which are now folded and hidden in the seemingly portrait-like image of the nucleotide as a simple genetic building block. M'charek (2014) shows that there are moments when a

nucleotide stops being a realistic portrait of a molecular process: the resequencing of the mitochondrial genome revealed an extra C in the original reference genome, which the scientists decided not to correct for pragmatic reasons, as it would have necessitated renumbering all the following loci in the reference genome. M'charek argues that through its continuing presence, the extra C points to the forgotten histories of construction underlying the reference sequence. Crucially, the extra C has the potential to unfold in unexpected ways at unexpected times. It thus encapsulates multiple socially and technologically shaped temporalities.

Queering Time

Seen from the vantage point of the present moment, evolutionary history appears as a continuum of seemingly endless generations across millennia. What connects generations is the act of reproduction. While many evolutionary approaches highlight the role of ecological and biosocial factors, such as scarcity of food, or social organization, reproduction appears nevertheless *retrospectively* as the tie that connects generations to the movement of evolutionary history from the past to the present (Oikkonen 2013; Roof 2007). This suggests that reproduction plays a key role in how evolutionary temporality is conceived as a means of imagining belonging.

The first chapters of this book showed that population genetic knowledge about roots and origins emerges through assumptions about reproductive ties such as the passing of mitochondria DNA through exclusively maternal lines of descent. But population genetics is entangled with reproduction and temporality also in terms of the larger cultural frameworks of how time is conceived. As population genetic knowledge is produced, invoked, and given meaning to within cultural discourses and practices, it is crucial to understand the connections between the reproductive underpinnings of evolutionary narratives and those of culture at large. Understanding these connections will shed light on how population genetic imaginaries of belonging achieve their rhetorical appeal as preferred ways of accounting for origins and destinies. To this end, I turn next to the theorization of the reproductive dynamics of temporality that

have emerged within and around queer studies. I am interested in the connection between normative assumptions of sexuality and normative arrangements of time, as well as in the possibility of imagining temporality differently.

One of the central concerns of queer theorists of temporality has been the predominant cultural assumption that time is linear, future-oriented, and progressive. This arrangement of time relies on a series of events that are assumed to naturally follow in a sequence. On the level of individual lives, the passage of time is conceived through events like birth, childhood, marriage, reproduction, and responsible middle age. This personal timescale has its parallel at the communal and national levels, as institutional forces "link properly temporalized bodies to narratives of movement and change" so that "people are bound to one another, engrouped, made to feel coherently collective, through particular orchestrations of time," as Elizabeth Freeman puts it (Freeman 2010, 3–4). In a similar vein, Tom Boellstorff highlights how the predominant understanding of temporality as linear and progressive is "shaped by linked discourses of heteronormativity, capitalism, modernity, and apocalypse," which structure the parameters within which identities, political acts, and communal belonging may emerge (Boellstorff 2007, 228). At the same time, scholars have argued that queer and other nonnormative practices are often organized by alternative conceptions of time. According to Jack Halberstam, such "queer time" may be embodied in "the dark nightclub, the perverse turn away from the narrative coherence" of expected life events involving marriage or maturity (Dinshaw et al. 2007, 182; see also Halberstam 2005). Furthermore, Freeman suggests that alternative temporal practices and experiences informed by "nonsequental forms of time" may render nonnormative lives, subjectivities, and forms of belonging "invisible to the historicist eye" (Freeman 2010, xi). These critiques of linearity and normative assumptions of reproduction are important for the analysis of evolutionary narratives, as evolutionary narratives rely on reproductive trajectories originating in the prehistoric past and reaching toward futurity. Such trajectories are prime examples of how individual lives become tied to a widely appreciated sense of time as unceasing, incontestable, and totalizing movement through prehistoric eras. At the same time, as we saw in the previous chapters, only those lives that conform with the

reproductive underpinnings of evolutionary narratives are rendered visible.

Scholars inspired by queer theory have also explored the relationship between nonnormative sexualities and futurity. Some have rejected altogether the possibility of opening the future for nonnormative identities and more inclusive forms of belonging. For example, Lee Edelman (2004) views the very idea of futurity as incompatible with queer politics. According to him, if society and culture are organized by "reproductive futurity" that foregrounds the image of the child as a promise of continuity, then "the queer comes to figure the bar to every realization of futurity, the resistance, internal to the social, to every social structure of form" (Edelman 2004, 4). Others scholars, like José Esteban Muñoz and Elizabeth Povinelli, have addressed the possibility of alternative futures. For Muñoz, queerness is characterized by "a longing that propels us onward" (Muñoz 2009, 1). Such longing refuses to accept current social, political and institutional practices and insists "on potentiality or concrete possibility for another world" (Muñoz 2009, 1). Povinelli, too, seeks to outline "the conditions in which new forms of social life emerge" by tracing moments and spaces through which alternative ways of organizing social ties, belonging and temporality could arise (Povinelli 2011, 5). Viewed in the context of evolutionary narratives, these analyses raise the question whether the reproductive dynamics through which evolutionary origins and genetic belonging are narrated could be challenged. Could evolutionary belonging be imagined in terms that defy assumptions of kinship that are based on heterosexual reproduction?

Apart from linearity and futurity, scholars have also explored the affective structures of the present. Reflecting the accounts of the past, present, and future as mutually entangled outlined above, scholars have argued that the boundaries of the present are blurry and shifting. For example, Carolyn Dinshaw theorizes "an expanded present, a temporally multiple now" (Dinshaw 2007, 112) that enables "a sense of simultaneous belonging to one's own time as well as to other times" (Dinshaw 2007, 119). At the heart of this conception of temporality is the role of the present moment in the dynamics of historical consciousness. For Dinshaw, the multiplicity of the present engenders unexpected and often unrecognized connections between communities and individuals across

historical time. These manifest in experiences of anachronism, "of time falling outside the apprehension of time that constitutes modern historical consciousness," that position people outside or against the sense of inevitable movement forward that characterizes hegemonic conceptions of time as linear (Dinshaw 2007, 111). The way in which the present achieves its sense of the now has also attracted critical analysis. For example, Lauren Berlant argues that "the present is perceived, first, affectively"—that is, through sensation, pulsation, intuition—before it becomes a series of events that can be narrated as part of historical processes (Berlant 2011, 4). The continuously ongoing negotiations over the shape and meaning of the present, including when and where it begins, organize how we orientate ourselves toward the past and the future, and how both intimate lives and communal experiences take shape as part of historical time.

These theorizations of the present as an affectively charged temporal arrangement shed crucial light on the imaginaries of roots and belonging that have emerged around population genetics. They draw attention to how we are located in the affective structures of the present as subjects of evolutionary knowledge. If what counts as past is defined from the present moment, as the observations above would suggest, are genetically framed projects of searching for roots and belonging engaged primarily with the affective appeal of the present rather than with knowing the evolutionary past? It is after all only through the present that the search for roots makes sense. Moreover, the idea of "a temporally multiple now" resonates with Amade M'charek's notion of folded objects. Together they shed light on how the temporalities of population genetics and evolutionary belonging fold and unfold in different situations.

Evolutionary History as Collective Memory

Population genetic temporalities are also closely connected to another aspect of cultural dynamics of time: collective memory. Memory studies scholars use the term *collective memory* to refer to the ways in which our

lives are embedded in, and take shape through, memories that are not based on personal experience. We rely daily on a host of collectively circulating memories of local, national, and global historical events. These events often include incidents and developments that are seen as defining moments for national or cultural communities, such as wars (both won and lost ones), declarations of national independence or regional autonomy, signing of constitutions or amendments, or nationally framed technological advances (e.g. the moon landing). As collective memories involve past events that are beyond the realm of personal experience, the circulation and maintenance of collective memories require practices of repetition (and often redefinition) through museum exhibitions, school textbooks, public speech acts (by politicians and public figures), or popular cultural products such as film or television. Viewed in terms of temporality, collective memories emerge from repeated acts of recollection and remembrance that bring the past in its myriad public and semi-public manifestations within the affective reach of the present.

I am interested in collective memory because cultural representations of population genetics and evolutionary roots often invoke the language of memory and remembrance. For example, James Chatters's account of the Kennewick remains and Bryan Sykes's account of the Cheddar remains quoted in the previous chapter invoked the idea of bones as a witness to evolutionary history. Such portrayals resonate with, and find support in, the idea of DNA as a molecular clock that records and remembers events that are too far in the past for humans to remember. This idea of DNA as a historical witness organizes not only discourses of ancient DNA but also accounts of DNA retrieved from our own cells. The mutations we have accumulated appear as a source of authentic, first-hand accounts of our origins. This extends the affective present (including the historical past that is connected to the present through collective memories) to prehistoric events. As such events have left no written documents and only a few material objects (such as rudimentary tools) and images (such as occasional cave paintings), DNA emerges as the primary tie that connects us to our evolutionary ancestors.

It is through this perceived role as a witness to the foundational events in the prehistoric tundra or savannah that DNA becomes entangled with collective memory. In popular discourse, DNA is often portrayed as *remembering for us* what we cannot remember. It is also assumed (though often more covertly) that through this displaced act of recollection we in fact come to remember what cannot be remembered. But how exactly does something that cannot be remembered become part of collective memory? The idea of *prosthetic memory* proposed by Alison Landsberg (2004) is useful here. Landsberg develops the concept in the context of twentieth-century mass culture. She argues that "technologies of mass culture and the capitalist economy of which they are a part open up a world of images outside a person's lived experience, creating a portable, fluid, and nonessentialist form of memory" (Landsberg 2004, 18). Landsberg highlights that such memories "no longer have exclusive owners; they do not 'naturally' belong to anyone" (Landsberg 2004, 18). In accordance with this observation, she approaches prosthetic memories as mechanisms located "at the interface of individual and collective experience" through which both individual subjectivities and collective forms of belonging take shape in relation to one another (Landsberg 2004, 19). Although Landsberg focuses on mass culture, the mutability and portability of prosthetic memory could also elucidate how DNA becomes a means of remembering prehistory. By remembering for us, DNA enables emotional time travel through which we can place ourselves in the imagined affective realm of the distant past. DNA, then, is not merely prehistoric memorabilia but also a mechanism through which past and present fold into one another constituting an affectively organized whole. This perceived role of DNA arises from the ambivalent nature of DNA as material and yet virtual. That is, DNA is a record of an evolutionary past as well as a mechanism, *the code of life*, through which new evolutionary realities—such as new presents and futures—can be produced and potentially rewritten.

This ambivalence renders DNA a powerful tool of prosthetic memory. The combination of abstraction and material uniqueness makes it remarkably fluid as an affective resource. This fluidity is strengthened by the imaginary scope that DNA promises. Associated with both nonhuman

characteristics such as remarkable endurance and perpetuity—the organizing principle of Dawkins's book—and human characteristics such as emotion and recollection, DNA appears as if being able to bring together mathematical and affective aspects of life across evolutionary millennia. DNA operates as a means of prosthetic memory primarily through popular cultural representations of genes and evolutionary history—the 1993 blockbuster movie *Jurassic Park* is an illustrative example. At the same time, these cultural representations are premised on the idea of DNA *itself* as a prosthetic tool of time travel. That is, the rhetorical power of cultural products such as films about evolutionary history arises from the epistemic authority and affective investments that DNA carries as a cultural symbol. As suggested above, DNA is a unique ontological entity in that it is simultaneously a historical object, a measuring tool, and the mechanism of producing life. In this, it differs from prehistoric objects such as stone tools or utensils made out of animal bones, which do not embody similar ontological multiplicity or epistemic prestige. For this reason, it is unlikely that these other objects could become means of extending collective memory to the evolutionary past with similar persuasive power.

The qualities of abstraction and inherent revisability posit DNA as if able to transgress time and space, and thereby connect the evolutionary past to the affective structures of collective memory. The abstract nature of DNA also appears to make it notably resistant to wear, requiring remarkably little updating and rhetorical work to maintain its affective appeal. At the same time, the widely accepted assumption that DNA is inevitably material—an assumption that contradicts the abstractedness of genetic knowledge—gives the recollections imagined through DNA a sense of irrefutability. Furthermore, the underlying tensions between DNA as making connections across time and space, and DNA as a material signature of individuality, render the meaning of "collective" in collective memory open. DNA connects us potentially to various types of imagined evolutionary communities depending on the level of differences and similarities at which scientists are looking. Because of this ambiguity, DNA can be integrated into mutually incompatible frameworks of collective memory seemingly effortlessly.

Evolutionary Nostalgia and the Prosthetic Dynamic of Longing

Both reproductive temporality and collective memory are crucial to the working of *evolutionary nostalgia*, the redrafting of the connection between past, present, and future into a multidirectional affective temporal dynamic. Evolutionary nostalgia relies on the assumption that there is a connection between the passage of time, unfolding evolutionary trajectories, and reproduction. It uses the reproductive underpinnings of evolution as a rhetorical resource that invest evolutionary trajectories with a sense of symbolic weight and epistemic primacy over other means of belonging. Evolutionary nostalgia also draws on the metaphorical power of DNA to extend the affective realm of collective memory to prehistory. This invests the evolutionary trajectories engendered through the reproductive logic of evolutionary temporality with considerable affective appeal. However, evolutionary nostalgia cannot be reduced to either reproduction or collective memory. What distinguishes evolutionary nostalgia as a mode of belonging is the *future-orientedness* of its affective grasp. In other words, while nostalgia appears to be about the past, it is in fact structured and motivated by persistent fantasies about how things could have been or could still be "if only." The concept of evolutionary nostalgia I am proposing here is in line with Turner's observation that the virtual and apparently timeless nature of Clayton's "genome time" provides a basis for nostalgic longing toward an imagined evolutionary past (Turner 2007, 59). As we saw in Turner's analysis of the temporality of cloning, the evolutionary past, preserved in the DNA in prehistoric bones, emerges as a location of possible alternative futures.

Before I explore and explicate the dynamic of evolutionary nostalgia through works of fiction, a short discussion of nostalgia is necessary. Considering the popularity of memory studies, it is no surprise that nostalgia has received considerable scholarly attention. Nostalgia is commonly understood as a form of longing for a past era or a lost place (Boym 2001; Muller 2007; Smith 2000). This place or time does not, however, have to be real or personally experienced, as nostalgia can be directed to an age or site that the nostalgic individual has never visited, such as the imagined geographic location or fantasized historical moment

from where one's family, community, or nation allegedly came from. In this sense, it fits considerably smoothly within attempts to narrate evolutionary roots through population genetics. Nostalgia is also characterized by temporal ambivalence, as the direction of longing is not always obvious. As Adam Muller observes, nostalgia "belongs neither to the present, the past, nor to the future, and yet it remains in some way attached to all three of these temporal zones" (Muller 2007, 739). Similarly, Svetlana Boym notes that "[f]antasies of the past determined by needs of the present have a direct impact on realities of the future" (Boym 2001, xvi). In other words, nostalgia relies on an imagined causal connection between past, present and future, so that implicated in the desired past is an alternative present and a previously unimagined future.

Like Landsberg's prosthetic memory, nostalgia operates at the interface between public and private. Indeed, nostalgia is one means through which prosthetic memory operates. Boym highlights that nostalgia always includes a collective dimension, which separates its logic from more personal emotions. According to Boym, "nostalgia is about the relationship between individual biography and the biography of groups or nations, between personal and collective memory" (Boym 2001, xvi). Furthermore, as a means of negotiating personal and collective experience, nostalgia is ultimately a structural dynamic. As Kimberly K. Smith puts it, nostalgia is "a particular way of ordering and interpreting the various ideas, feelings, and associations we experience when thinking of the past" (Smith 2000, 509). Narrative is a key mechanism through which this structural dynamic operates. Nadine Attewell captures the centrality of narrative when she describes nostalgia "as this longing for the certain shapes the past assumes as history, as narrative" (Attewell 2004, 44). Read in the context of Boym's observation about the implicit future-orientedness of nostalgia, it could be added that the shape of narrative that history takes also involves a specific rewriting of the narrative shape of the future.

Nostalgic longing is often perceived as irrational because its fantasies about returning to a long-gone past appear to contradict the progressive, future-oriented ethos of modern society. Attewell observes that this equation of nostalgia with irrationality reinforces the idea that nostalgia is practiced and cherished in "lower" forms of culture. In particular,

nostalgia becomes linked with "sentimentality and a degraded popular culture, and hence with genres—the formulaic romance, for instance—coded as feminine" (Attewell 2004, 23). For this reason, cultural texts that craft an affective continuum between the present and the evolutionary past through narratives involving romance, intimate relationships, or emotions provide insights into the ways in which evolutionary history becomes a means of imaging and enacting belonging in contemporary society. I turn now to two works of fiction that thematize evolutionary history in order to elaborate on the complex entanglements between evolutionary temporality, nostalgia, romance, and reproduction. The first of the novels, archeologists Kathleen O'Neal Gear and W. Michael Gear's popular historical novel *People of the Raven*, is structured around a romantic narrative. As romantic narrative is literally organized by longing, the novel is particularly suited for an analysis of how evolutionary nostalgia operates.

Longing for the Future in the Past

Published in 2004, *People of the Raven* is a response to the cultural controversy and legal battle surrounding the Kennewick remains since 1996. The novel imagines the prehistoric circumstances of Kennewick Man's life by portraying a growing conflict between two prehistoric groups of people within what is today Washington State. The book uses evolutionary nostalgia as a means through which the animosity and cultural differences between the two groups are eventually erased and embedded within an affectively charged trajectory of evolutionary progress. While the novel does not invoke the language of genetics, its attempt to imagine prehistoric life through ancient bones draws on, and resonates with, the idea of DNA as a historical witness. Echoing the witnessing power of DNA, evolutionary nostalgia appears to bridge the gap between history and prehistory through the temporal trajectories it produces between evolutionary origins and the present.

People of the Raven advocates openly for the claim made by plaintiff scientists in the Kennewick controversy that scientists should be allowed to study prehistoric human remains. The book's foreword argues fiercely

for the scientific study of the Kennewick remains, and the fictional epilogue imagines the final moments of intense study in the basement of a scientist's home before authorities arrive to collect the prehistoric human remains. This scene resonates with the similar scene in James Chatters's *Ancient Encounters* discussed in the previous chapter; only this time the scientist is female and part Native American, a narrative strategy that functions to disassociate science from privileged Euro-American masculinity. Echoing Chatters, the epilogue claims that the intended repatriation would remove the remains "out of context with his past" by sidestepping the concerns of national and continental history (Gear and Gear 2005, 7). It portrays the repatriation of ancient human remains to Native Americans strikingly as "a form of murder" (Gear and Gear 2005, 11). This portrayal equates the refusal to prioritize knowledge produced through the epistemic apparatus of Euro-American science with the actual death of an ancient people. Such an equation engenders an image of annihilated future, as the perceived future-orientedness of Euro-American science is seen as being replaced by the assumed past-orientedness of Native American knowledge. Yet the book seems to wish to reconcile the viewpoints of modern science and Native American heritage, and it does describe many aspects of past Paleo-Indian cultures with celebration.

In terms of plot, the book traces the destinies of two racially distinct peoples who struggle for survival in an increasingly harsh environment. The North Wind People are the firstcomers in the area, and their chief Cimmis is Kennewick Man—although the posthumous name is never mentioned in the narrative. However, the novel focuses on the Raven People, who rise to resist the raids, murders, and rapes by the North Wind People. The novel's narrative ties the accelerating destruction of villages and the struggle for power within the two communities to the developing romance between the Raven leader Rain Bear and the former North Wind matron Evening Star. Predictably, the story ends with the banishment of the North Wind leaders (including the wounded Cimmis), the first stages of peace between the tribes, and Rain Bear and Evening Star's union, thereby celebrating collaboration and unity—both ethnic and heterosexual. The novel is indeed formulaic and faithful to the genre conventions of popular romance. Yet the affective and temporal structures

that organize its narrative provide an intriguing entry point to the cultural appeal of evolutionary accounts of belonging.

Through its focus on the gradual erasure of differences between the two prehistoric groups, the novel invokes the idea of diversity—of opinion, culture, ethnicity—as an only temporary obstacle that can be overcome. Crucial to this narrative dynamic is the portrayal of prehistoric origins as heterogeneous (as represented by the two prehistoric peoples) rather than single and unified. In the novel's prehistoric narrative, this heterogeneity is then replaced by unity. Crucially, this emphasis on heterogeneous origins casts the prehistoric struggle between the Raven and North Wind peoples as parallel to the current epistemic struggle over the correct account of American origins. As a result, the past battle between the two prehistoric groups appears as both a narrative reenactment and a historical predecessor of the modern struggle between scientists and Native Americans. This narrative strategy equates imagined North American prehistory with US national history, as the present sets the framework within which the past is interpreted. It also casts the present as no wiser than the past, as suggested by the tension between ethnically marked communities—in this case, the symbolically white scientists and the symbolically never-quite-modern Native Americans. The narrative of future communal coherence that the novel's prehistoric story envisions, then, is a failed narrative, as it does not deliver what it promises.

Yet the past is imagined as a source of wisdom in order to imagine an alternative present and future. This is where nostalgia enters the picture. The present that the novel's prehistoric narrative seeks is not necessarily our present, nor is the future it envisions the future that will emerge from our current reality. Rather, it is an alternative present and future untouched by epistemic and cultural struggles between racialized groups. This becomes evident in a scene where Rain Bear decides not to kill an evil North Wind healer who travels with his blind son through Rain Bair's village. When the healer leads the massacre of another Raven village, Rain Bear doubts his earlier decision. Evening Star, however, responds:

> Then the boy was the key to the Raven People's future. And it's the future that you must face. Your people need to be shaped and molded. The story is told that when you came to this land, it was as a few scattered clans,

> loosely affiliated, and then only by your language. Canoe load by canoe load, you drifted down from the north, hunting, and moving on. Is that what you wish to be forever? (Gear and Gear 2005, 190)

This invocation of origins suggests that roots are important in rethinking the future, and that change is necessary so that the narrative of the prehistoric people (and, by implication, the contemporary nation at the other end of evolutionary history) may produce a satisfactory trajectory. It also posits the future as the ultimate object of nostalgia, while imagining the beginning of the narrative as a promise of continuity. This connection between imagined origins and fantasized destinies is invested with a sense of causality that renders the alternative present and future paradoxically both impossible and logically necessary. At the same, the unresolved question of both past and present racialized and cultural differences disappear from the narrative focus.

Rain Bear and Evening Star's sexual union becomes the locus of this nostalgic longing. The romance plot is a convenient tool for nostalgia because romance actualizes the promise of futurity. That is, romantic narrative is structured on a search for a union, which in turn carries symbolic weight as the perceived mechanism through which happiness, belonging, offspring, and communal continuity are produced.[1] The formulaic patterns through which the protagonists' love story develops—immediate attraction, intense dialogue, mutual doubt about the relationship—produce a sense of recognition and predictability. The reproductive underpinnings of both romance and evolutionary narrative become evident toward the end of the book, when the Raven leaders decide what to do with their enemies. Rain Bear argues that the North Wind leaders should not be killed:

> Don't you understand? It's our families that we're talking about. If we choose the wrong path today our sons and daughters will continue to kill each other until we are all so weak the Cougar People or the Buffalo People will move into our lands, and we will be *their* slaves. (Gear and Gear 2005, 535; emphasis original)

This invocation of "our sons and daughters" implies that both evolutionary and romantic narratives produce offspring. The literally

reproductive union of Raven and North Wind men and women, represented by the two protagonists' marriage, thus places heterosexual reproduction at the heart of the invoked evolutionary narrative. As Lee Edelman (2004) observes, the image of the child we repeatedly encounter in cultural discourse stands for "reproductive futurity," the pervasive assumption that children are our only route to futurity. Heterosexual desire in *People of the Raven* thus promises both reproductive futurity (children, future generations) and narrative continuity (a future-oriented temporal trajectory), thereby structuring evolutionary belonging in foundational ways.

Evolutionary nostalgia in *People of the Raven*, then, operates through assumptions of reproduction. Reproduction—understood both literally and symbolically—emerges as the tie that connects the opaque prehistoric past to the affective structures of the present. The symbolic weight attached to reproductive unions invests the connections engendered between past, present, and future with widely resonant cultural appeal. At the same time, the implicit future-orientedness of reproduction detaches nostalgia from a stubborn attachment to an unlivable past and associates it instead with a commitment to a better present and future. The symbolic weight of reproduction reinforces the idea that personal, communal, and national trajectories of evolutionary belonging are parallel, entangled, and compatible. However, as my analysis of the multiple forms of belonging produced through Cheddar Man suggested, such compatibility is illusionary. Furthermore, the seemingly easy parallelisms between personal and communal narratives of evolution mask the discrepancies between nonnormative experiences and practices traced by queer scholars like Halberstam and Freeman, and the apparently unceasing movement of historical narrative. To put it slightly differently, while one of the functions of evolutionary nostalgia is to bring prehistory within the affective structures of the present, the act of crafting those temporal connections erases experiences of temporality and belonging that do not conform with normative conceptions of time as future-oriented and reproductively organized.

These exclusions of alternative experiences of belonging suggest that although evolutionary nostalgia is quite complex in terms of its organization—it operates through two-directional temporal movement

and insists on the possibility of an alternative present and future—its effect seems to be totalizing. That is, evolutionary nostalgia appears as if it was the only meaningful way of organizing belonging. At the same time, it erases or domesticates heterogeneity, thereby masking unresolved questions about racialized identities and epistemic differences. This insight is crucial for understanding how evolutionary nostalgia operates as a means of collective remembrance: if evolutionary nostalgia is a prosthetic technology of collective memory, its ways of remembering are limited. As the narrative politics of *People of the Raven* suggests, such limitedness might be desired if one wants to turn prehistory into an affective resource for imagining coherent communities and trajectories of belonging that are uncomplicated by racialized, gendered, or sexualized differences.

Unfolding Temporalities, Intersecting Differences

My reading of *People of the Raven* suggests that evolutionary nostalgia is a rhetorical tool that draws on affective investments, cultural conceptions of temporality, discourses of reproductive futurity, the perceived significance of collective memory, and ideas of racialized and gendered differences. But what are the limits of evolutionary nostalgia as a rhetorical tool? What are the implications of its ways of crafting affective ties between the present and the distant past for how belonging can, and cannot, be imagined? Margaret Drabble's novel *The Peppered Moth* provides an illuminating starting point from which to explore these questions. *The Peppered Moth* is organized around a narrative about the intergenerational relationships between three women—mother, daughter, granddaughter—and thus it falls within the topics conventionally considered as feminine and associated with emotionality and sentimentality. Evolutionary nostalgia plays a central role in the novel, as the narrative crafts affectively charged multidirectional connections between the past, present, and future. But the novel is also a serious attempt to think the effects of population genetic inquiries into the past on gendered, classed, and racialized imaginaries of belonging. Indeed, the narrative politics of the

novel complicates the smooth operation of evolutionary nostalgia as a means of bringing us all within the affective web of collective memory.

The Peppered Moth was first published in 2000 around the time when the Human Genome Project and advances in genetic technologies had gained considerable cultural attention. It examines the complicated dynamics of cultural and biological inheritance between three generations of women. The oldest of the women, Bessie, was raised in the industrial South Yorkshire of the early twentieth century; her daughter Chrissie has settled into a peaceful and comfortable life in Oxford after a disastrous first marriage; and Chrissie's daughter Faro is a London-based science journalist now in her thirties. The novel asks how the three women have become who they are, and to what extent their choices arise from environmental influence, social pressure, biological inheritance, pure coincidence, or conscious and voluntary choice. Drabble uses DNA as a prism through which she develops these questions. The present moment of the novel centers around granddaughter Faro's work assignment in South Yorkshire, where she is writing on the connection between the ancient skeleton known as Cotterhall Man discovered close to Breaseborough and Cotterhall where Faro's maternal grandparents grew up, and the analysis of DNA from members of families with roots in the area, including Faro and her great aunt Dora. Conducted by molecular scientist and media wizard Dr. Hawthorn, the genetic analysis seeks to establish a direct mitochondrial connection between Cotterhall Man and the local residents. In this respect, the novel echoes closely the case of Cheddar Man explored in the previous chapter.

In *The Peppered Moth*, mtDNA takes on a metaphorical role as the ultimate tie that roots us in the past. In the novel, mtDNA appears to be able to create connections that extend beyond the science of mitochondrial DNA. For example, the novel associates mtDNA with inherited behavioral patterns, ways of experiencing the world, or characters' choice of profession or partner. The novel also employs scientific models in ways that are not supported by science. For example, the novel portrays mtDNA as if it was a product of natural selection, even though population geneticists are often interested in noncoding sections of mtDNA that are not under clear selective pressure. The novel uses repeatedly words familiar from Darwin's theory of natural selection such as "adapt" or "survive," as

when the narrator ponders whether groups of people moving within the region had "adapted" to their new surroundings (Drabble 2001, 165), or suggests that Bessie's childhood friend Ada "will survive, we may feel sure, for she is robust" (Drabble 2001, 43). Bessie emerges as the opposite of Ada through Darwinian discourse: a sensitive and physically fragile girl, "Bessie may be an evolutionary mistake, a dead end, a throwback to the clear valleys. Natural selection may de-select her" (Drabble 2001, 8). The metaphorical nature of such invocations of evolution is made clear, for example, when the discourse of mutation is extended from genes to people, as when the narrator states that "Bessie did not mutate" (Drabble 2001, 115). Crucially, such metaphorical use of scientific terminology is more than just an inaccurate representation of science: it draws attention to the fact that the discourses surrounding mtDNA and the figure of Mitochondrial Eve were entangled with rampant cultural imaginaries from the very beginning, as my analysis in Chap. 2 suggested. The novel's metaphorical use of mitochondrial inheritance to conceptualize kinship and belonging beyond science invests the idea of evolutionary rootedness with considerable affective power.

The metaphorical use of DNA in the novel centers on the extent to which our choices are determined or influenced by genetic, social, and environmental factors, represented in the novel by the dirt and depression of the mining town of Breaseborough. For example, Chrissie's father Joe is portrayed as "beginning to dread the genetic trap" when watching his daughter grow up, as if the past he and Bessie left in South Yorkshire was going to claim their daughter (Drabble 2001, 184). When, in the novel's present, now-retired Chrissie visits Australia, she looks for the place where her father's sister Ivy had emigrated decades earlier. Watching the beautiful landscape, Chrissie concludes that "Ivy had escaped," yet she ponders on her own choices in quite different terms: "you just can't get away from your own past, can you?" (Drabble 2001, 351). The novel is organized around an unresolved ambivalence as to what kinds of forces—biological, environmental, psychosocial, or forces of our own making—direct our lives.

The Peppered Moth deploys a dynamic of evolutionary nostalgia that is similar in many ways to the one mobilized in *People of the Raven*. Echoing the public discourses surrounding Cheddar Man, Drabble's novel posits

Cotterhall Man as a longed-for ancestor who will root the people of South Yorkshire in the prehistoric landscape of presumably authentic belonging. At the same time, those prehistoric origins emerge as a site through which the conditions of the present and the future are reevaluated, redefined, and enacted differently. That is, the very quest for genetic knowledge about the past is understood as producing forms of belonging and kinship that reshape the ontological parameters of the affective present. As in *People of the Raven*, this ties the present, the historical past, and the prehistoric origins into an affectively organized and seemingly seamless continuum. However, the ways in which the novel consistently highlights the ambivalence about determinism and voluntary choice undermines the power of evolutionary nostalgia to engender new alternative presents. In other words, it challenges the determinist and totalizing undercurrent implicit in evolutionary nostalgia. Whereas evolutionary nostalgia in *People of the Raven* made the reimagined trajectory between the past and present appear inevitable as if it was the only meaningful way of belonging, the ambiguity about determinism in *The Peppered Moth* opens up the reimagined present and future to multiple mutually contradictory discursive registers and imaginaries. This complicates the ways in which the past can be used to reimagine the present and future, and thus the seemingly straightforward dynamic of longing and belonging that emerged in *People of the Raven*.

The ambivalence about determinism structures how temporality operates in *The Peppered Moth*. The question of determinism emerges as entangled with multiple, coexisting temporal orientations that challenge the smooth two-directionality identified in *People of the Raven*. First, *The Peppered Moth* portrays DNA as carrying the past, as when the narrator raises the possibility that "memories lingered in the bone, in the tissue, in the DNA of the Cudworths, the Barrons, the Badgers" (Drabble 2001, 70). Instead of DNA simply recording the past—the central idea of the molecular clock—the past emerges as having an enduring *affective* presence in the DNA as lingering recollections of past experiences. Second, the question of determinism complicates the idea of evolution as forward movement. When Bessie's working-class parents are faced with growing evidence of their daughter's academic talent, the episode is described in relation to evolutionary temporality: "How can they have produced this

swan child? Is she a freak, *a throwback, a throw-forward*?" (74; emphasis mine). Similarly, people may behave in unexpected ways that contradict the logic of evolutionary progress, yet the novel insists that their behavior cannot be separated from the evolutionary past and the working of evolutionary forces:

> Human beings were opaque, amazing, in their leaps, their motivations. And yet there were links, *reaching backwards into cavernous recesses of time itself*, into the limestone, into the potholes, into the caverns. How could one begin to follow the leaps? Did families remain static for centuries, then suddenly, in an instant, in a generation, mutate? Did whole cultures leap and surge? (Drabble 2001, 159; emphasis mine)

Even though the novel centers on direct ties between generations (represented by the mitochondrial connections between the three female characters), the forward movement of evolutionary temporality is complicated by leaps, gaps, changes in tempo, and even moments of return to the past.

These temporal complications find further support in how evolutionary history emerges as temporal distance that materializes in the present in unexpected ways. When Bessie visits her dying mother, the millennia that separate modern humans and the prehistoric past suddenly emerge as if separating the two women: "And there they sat, mother and daughter, looking at one another. There was nothing to be said. The silence was stiff and solid. Thousands of years of silence lay banked up behind them, lay coldly between them. There were no words. It was as though language had not been invented" (Drabble 2001, 201). Another key event takes place at the end of the novel, when a spontaneous fire caused by the gasses hiding in the now-closed mines destroys the recently opened local history and nature center and the site where Cotterhall Man was discovered: "It was the ancient poison that had broken out," the narrator tells us (Drabble 2001, 378). In this explosive and unexpected event, the connections between the present, the historical past (the gasses resulting from mining), and prehistory (the imagery through which the history of mining is rendered "ancient") do not constitute a straightforward temporal continuum. Instead, the past is a potentiality that may rupture the

present, pause it, or push it toward unforeseen futures. This is a clearly more violent and disarrayed dynamic of temporal relations than the two-way longing that organizes evolutionary nostalgia in *People of the Raven*.

This plurality of temporality shapes the forms of evolutionary belonging that emerge in *The Peppered Moth* in crucial ways. Toward the end of the novel, Faro finds out that there is a direct mitochondrial connection between her (and, by implication, Chrissie and Bessie) and Cotterhall Man. This suggestion of apparently straightforward personal belonging is complicated by repeated references to communal or regional belonging: the novel is, after all, a history of a region and a community—an early twentieth-century South Yorkshire mining town—as much as it is a history of three women. In this respect, the novel echoes the tension between personal and regional belonging in the media coverage of Cheddar Man discussed in the previous chapter. However, the thematization of temporal plurality—leaps, gaps, intensifications, moments of return—in *The Peppered Moth* complicates the idea of parallel evolutionary trajectories of personal, communal, and regional belonging. Moments of temporal multiplicity in the text suggest that different personal, communal, regional, and national forms of belonging emerge through one another, and that these entanglements of belonging draw on and mobilize intersectional differences. For example, the way in which evolutionary millennia fall between Bessie and her dying mother in the quote above mobilizes gendered kinship as well as articulations of class: her mother's death brings Bessie from the clean and leafy upper-middle-class suburbs of Kent in the South of England to her childhood's grime-covered working-class South Yorkshire her mother never left behind. Similarly, the rupture of the present by the forces of the past in the explosive fire described above mobilizes classed, gendered, and racialized differences that underlie the history of mining. It is as if the systematic exploitation of the health and safety of workers and their families by rich mine owners came back to haunt the present, to remind us that the seeming progressiveness of evolution relies on inequalities and systematic abuses of power.

What makes *The Peppered Moth* particularly interesting for my analysis is the way in which it renders visible the mutual entanglement of class and race in evolutionary discourse. In a key scene set in the 1920s, we see the industrial landscape of South Yorkshire through the eyes of a Londoner

on the train across the country: "The pitheads, the quarries, the scars, the mountains of slag, the spoil heaps, the careless, casual filthy dumping. The lack of the most elementary, animal cleanliness. You could not get away from it—the lack of *toilet training*. Not even animals foul their own nest as this northern race had done" (Drabble 2001, 93; emphasis original). This poignant description brings together several categories of difference. It invokes the boundary between human and nonhuman familiar, for example, from the long history of employing ancient human remains to construct national narratives. Intriguingly, it posits the view from the train window as being even beyond animal behavior. The description also invokes the idea of immaturity through language of "toilet training." Furthermore, it operationalizes simultaneously both class and race: the condemnation of the "northern race" suggests that the people of the area—primarily working-class families employed in the mines—are essentially different from the human population in the south of the country. The assignment of responsibility to the local population for the perceived regression is also inherently problematic in that the people directing the destruction of the landscape were mostly rich mine owners and their managers. The description of the desolate view from the train situates these intersecting categories of difference within an evolutionary framework in which they stand (for the visitor on the train) for the failure of evolution to engender progress. In doing so, the scene draws attention to how class has been racialized and how race has been classed in narratives of evolutionary history.

Descriptions like this suggest that the unifying tendencies of evolutionary nostalgia—the longing for the past as a source of a revised present and future—do not manage to tame the entangled intersectional differences that underlie evolution as a means of belonging. Likewise, although evolutionary nostalgia constitutes a powerful way of connecting the past, present and future, it is not able to do away with temporal ambiguity, the coexistence of alternative ways of organizing time as cyclical, punctuated, stationary, or potentially eruptive. In *The Peppered Moth*, multiple temporalities, multiple forms of belonging, and multiple underlying differences emerge as entangled and inseparable. The thematization of alternative temporalities renders visible the ways in which one form of belonging (such as personal belonging) is entangled with other forms of

belonging (such as communal or regional belonging). The multiple coexisting temporalities also highlight the historical constellations of intersecting differences—especially, gender, class, and race—that underlie personal, communal, regional, and national evolutionary belonging. This indicates that personal, communal, regional, and national forms of belonging do not constitute parallel, separable evolutionary trajectories but are intertwined and constituted through one another.

Finally, the metaphorically charged DNA of *The Peppered Moth* resembles the "folded object" theorized by M'charek in many ways. While M'charek discusses the construction, circulation, and reevaluation of a scientific object—a reference genome—in scientific practice, her observations as to how an object unfolds differently in different situations revealing different sequences of events provides a way of conceptualizing the temporal politics of population genetic knowledge also *metaphorically*. As a folded object, DNA in *The Peppered Moth* acquires a prosthetic quality that resonates with the idea of prosthetic *memory* theorized by Landsberg. In *The Peppered Moth*, the genetic link between Cotterhall Man and the three women becomes a prosthetic device through which evolutionary history and belonging unfold differently at different times and in different situations. Arising from the metaphorical resonances of genetic discourse, DNA carries these alternative affective histories as potentialities that may unfold—sometimes simultaneously. The final sections of this chapter reflect on these two phenomena—the unfolding of multiple evolutionary histories and the prosthetic nature of DNA—in relation to the affective dynamic of evolutionary nostalgia and the emergence of evolutionary belonging.

The Obamas, and the Making of Unity Through Genetic Trajectories

When Barack Obama was elected the 44th president of the United States in 2008, his racial and ethnic ancestry received intense public scrutiny. So did the ancestry of Michelle Obama. As the successful election campaign turned the Obamas into symbols of the present state of the nation, both

liberal and conservative commentators and media outlets sought to define the ways in which the Obamas belonged to the American historical continuum. Some conservatives highlighted the "foreign" status of President Obama's Kenyan father, thereby framing Obama as not truly American. Others highlighted Michelle Obama's African-American roots and the way in which her family history is entangled with key events in American history, such as the abolition of slavery, the civil rights movement, and the movement of African-American families from the south to the north.

Not surprisingly, some of the attempts to trace the genealogies of the Obamas turned to DNA for evidence. While neither the president nor the first lady provided DNA samples (nor expressed support for these genealogical endeavors), genealogists used DNA collected from distant relatives to construct intergenerational trajectories of belonging to root the first couple in the momentum of US history. I turn now to two of these studies to explicate how the temporal structures of nostalgia and the idea of genetic kinship organize the ways in which belonging is enacted in contemporary culture. In particular, I elaborate on the idea of DNA as the location of multiple, potentially unfolding histories, and the ways in which those histories are entangled with ideas of difference and sameness.

In June 2012, the *New York Times* published an article titled "Meet Your Cousin, the First Lady: A Family Story, Long Hidden" by journalist Rachel L. Swarns (Swarns 2012). Based on Swarns's then-forthcoming book *American Tapestry: The Story of the Black, White and Multiracial Ancestors of Michelle Obama*, the article suggests that Michelle Obama's maternal great-great-grandfather Dolphus was the son of Charles Marion Shields, whose father owned Dolphus's mother Melvinia during the years leading to the Civil War. While previous genealogical research had already established Dolphus and his mother Melvinia as Michelle Obama's direct ancestors, Swarns made the claim that DNA collected from Michelle Obama's black relatives, who descend from Dolphus and Melvinia, and the white Shields who descend from Charles Shields and his wife, showed that the two Shields families were genetically linked. Furthermore, Swarns argued that based on genetic evidence, Charles (rather than his father Henry) was the most likely father of Melvinia's son Dolphus.

A month later, in July 2012, the *New York Times* published an article on President Obama's genetic inheritance, written by journalist Sheryl Gay Stolberg (Stolberg 2012). Titled "Obama Has Ties to Slavery Not by His Father but His Mother, Research Suggests," the piece explains how a research team at the genealogy company Ancestry.com had studied Obama's maternal ancestry and had concluded that one line of his family led back to a seventeenth-century slave, John Punch, in Virginia. Punch had been an indentured servant, but when he was captured after escaping to Maryland, his servitude was extended for life. The article portrays Punch as "one of the first documented African slaves in the United States," who received his sentence years before slavery was officially established in Virginia. As with the case of Michelle Obama, the article invokes DNA analysis as a key means through which the roots of President Obama's mother's family could be established.

Both articles mobilize a temporal dynamic that is very similar to the dynamic of evolutionary nostalgia that structured the narrative politics of *People of the Raven*. While the two *New York Times* articles do not refer to evolutionary origins, they embed the idea of origins within a discourse of genetic belonging. In both texts, the previously unknown roots of the first couple are rendered as something that needs to be connected to the affective framework of the present. The longed-for past is established as a source of an alternative present and future that will recognize and celebrate the multiethnic origins of contemporary Americans as a sign of unity and coherence. The past, that is, emerges as the location of futurity. At the same time, the past, present, and future are connected through two-way linear movement: from the present to the past to an alternative present and future.

In Swarns's article, genealogical research engenders unexpected trajectories of genetic inheritance between Michelle Obama and Charles Shields on the one hand and the modern-day white Shields and Michelle Obama's biracial ancestor Dolphus Shields on the other. These unexpected trajectories from the present to the past become portrayed as a foundation for a new, harmonious American present. The article maintains that "[c]ontemporary America emerged from that multiracial stew, a nation peopled by the heirs of that antagonizing time who struggled and strived with precious little knowledge of their own origins. By 1890,

census takers counted 1.1 million Americans of mixed ancestry" (Swarns 2012). The text insists that this unacknowledged history is not just the history of African Americans, but also that of white Americans, who—like the white Shields—are related to African-American families through foundational moments in the national and regional past. Such moments in the past emerge as an affective source that, ideally, shapes the present, as when Mrs. Tribble, a member of the white Shields family, sees the picture of Dolphus Shields in a newspaper: "Mrs. Tribble never had any doubts about her family's ethic background. Yet when she stared at the photograph that day, she said she felt something entirely unexpected: a strong stirring of recognition" (Swarns 2012). It is a recognition of belonging, of the present connecting to the past, which in turn connects to a new, affectively different present.

Similarly, the second *New York Times* article embeds President Obama, and the symbolic weight of the presidential institution, in foundational moments of American history—the very establishment of slavery (Stolberg 2012). These forgotten moments come to redefine the present and the future. Like Swarns's article, the piece shows that seemingly white Americans like Obama's mother may have slave ancestors, and that two lines of the same family—one in Virginia living as "white" and another in North Carolina defined as "mulatto" in historical records—both carry African genetic ancestry arguably traceable to Mr. Punch, the seventeenth-century African slave. The claims of connecting the president to one of the "first" slaves before slavery echoes the privileging of temporal primacy in evolutionary discourse: the older the origins, the more valuable they are as an affective source of belonging. At the same time, the temporal primacy of those origins implies that the present and the future could be imagined and enacted differently using this newly found multiracial past as a foundation. Furthermore, crucial to how evolutionary nostalgia operates in both articles is the totalizing tendency of its temporal longing. Through the act of reimagining and reenacting the present, evolutionary nostalgia erases tensions between racialized categories of difference. While both articles celebrate racial and ethnic heterogeneity, the temporal dynamic of evolutionary nostalgia domesticates that heterogeneity under idealized unity and national coherence that seemed previously unachievable.

In both articles, evolutionary nostalgia operates through reproductive ties. Echoing the privileging of linearity in evolutionary discourse, the texts highlight the genetic trajectories between the Obamas and their direct ancestors: Barack Obama is the 11th great-grandson of Mr. Punch and Michelle Obama is the great-great-granddaughter of Dolphus Shields. This focus on linear trajectories posits reproduction as the implicit foundation of kinship and belonging. Moreover, reproduction emerges as entangled with temporality, as it constitutes the mechanism that pushes the rediscovered past toward an alternative present and future. Reproduction is affectively charged not only in terms of its perceived ability to engender belonging, but also in terms of its perceived ability to promise continuity and unity. This temporal dynamic is familiar from the invocation of romantic union in *People of the Raven*. It also resonates with queer critiques of the reproductive underpinnings of cultural conceptions of time and futurity.

In this reproductive temporal dynamic, cultural assumptions about the entanglement of temporality and reproduction, and evolutionary discourses of reproductive continuity through millennia, reinforce one another, giving the idea of genetic trajectories spanning through American history a sense of foundational and undeniable significance. What makes this reproductive temporal dynamic particularly striking is that it erases questions of love and emotional intimacy. In Swarns's piece on Michelle Obama, the reproductive links running from Henry Shields through Charles Shields and Melvinia Shields to Dolphus Shields remain *ontologically unchanged* notwithstanding whether Charles raped Melvinia or whether she consented. While the likely rape emerges as a source of anxiety and concern in the article, these emotions do not undermine the reproductive trajectories that enable evolutionary nostalgia to turn the newly discovered past into a promise of a better future. The foundationality and primacy of reproductive ties is further reinforced through the use of words like "kinship" and "family" to describe two groups of people that share very little prior to the revelation of their genetic connection. This suggests that reproduction, temporality, and belonging are entangled so thoroughly in cultural imaginaries that the entanglement has gained an appearance of naturalness.

Both articles highlight the role of DNA as a key means through which the past becomes integrated into the affective dynamic of the present. While both cases rely on archival work and traditional genealogy, genetic testing is portrayed as revealing the unexpected or providing ultimate evidence unachievable through other means. In the article on Michelle Obama, DNA samples collected from Charles Shields's official descendants and from Dolphus's descendants posit Charles as Dolphus's father. In the article on President Obama, an online genealogical and genetic database maintained by Obama's mother's extended family provides evidence that men in the seemingly white family have a "sub-Saharan" Y chromosome associated with Cameroon in Africa. In these instances, DNA resembles the folded object theorized by M'charek. In both articles, DNA appears to have the ability to unfold in unexpected ways so that previously concealed histories—the connections between African-American and European-American families, and the multiracial background of both families—become visible. These unfolding histories differ from the histories traced by M'charek in that they are presumably condensed in the molecular detail of the genetic material carried in the cells of living human beings rather than folds in a reference genome. Both Swarns's and Stolberg's articles appear to be informed by a progressive ethos that insists that science will have the power to unfold further stories of roots and connections still hidden in the DNA.

But DNA does not only reveal hidden histories, it also engenders them. Perhaps unintended by Swarns and Stolberg, the two articles portray how DNA becomes a means of enacting a new unfolding present in specific situated circumstances that involve particular methods of comparison or particular cultural vocabularies. It is through this situatedness that DNA is able to unfold into novel histories about the Obamas and their ancestors. This implies that DNA could unfold differently in different situations, for example, through different historical or regional comparisons. This in turn would generate different unforeseen histories and thereby enact different forms of belonging. Interestingly, this inherent situatedness of DNA challenges the totalizing tendencies of evolutionary nostalgia: the ways in which DNA can engender patterns of difference and sameness are situated and context dependent. Yet the two

articles appear to insist on the irrefutability of genetic information, as they rely on the smooth operation of evolutionary nostalgia as a means of generating temporal movement toward national coherence and unity.

This insistence is supported by the symbolic power of DNA. As in *The Peppered Moth*, DNA is seldom specified in the two articles: the only time we learn about the type of genetic material or analysis used in the genealogical studies is when Stolberg reports that President Obama's mother's extended family found an African Y chromosome. This vagueness makes it possible for DNA to take on a host of cultural, communal, and historical meanings that extend beyond the actual scope of any technique of genetic analysis. The vagueness about genetic techniques also blurs the line between different levels of belonging. As the interpretative power of DNA appears to encompass a range of societal and cultural phenomena, the line between personal, communal, and national belonging becomes increasingly blurry. This seemingly contradictory combination of flexibility and situatedness makes DNA a powerful tool of collective memory and cultural narratives of belonging.

The Many Sides of Evolutionary Temporality

This chapter has investigated the role of temporality in how population genetics and evolutionary imaginaries engender belonging. I have argued that genetic knowledge about human evolutionary past is entangled with the temporal structures of nostalgic longing, future-oriented movement, and the affective dynamics of collective memory. I have examined this entangled constellation of time, movement, affect, and memory in an admittedly roundabout way. I have turned and twisted it around many times, approaching it from slightly different (albeit related) angles provided by previous scholarship on the temporality of genes, genetic sequences as folded objects, reproduction and normative temporalities, and collective and prosthetic memory. Furthermore, I have traced this temporal constellation through specific textual formations including two novels, *People of the Raven* and *The Peppered Moth*, and two newspaper articles on the Obamas. Each of these texts captures crucial aspects of

how evolutionary belonging mobilizes and emerges trough temporality. Instead of trying to separate elements of temporality, affect, or memory, I have sought to illuminate the intricate ways in which they intersect and define one another.

The chapter has focused on a temporal dynamic that I have identified as central to contemporary evolutionary discourse: *evolutionary nostalgia*, the longing for the past as a source for imagining and enacting an alternative present and future. I have argued that this dynamic is rhetorically appealing because it appears to connect the distant past into the affective present while engendering a sense of coherence, unity, and purpose, as we saw in *People of the Raven*. At the same time, this totalizing tendency of evolutionary nostalgia erases or trivializes differences involving race, gender, sexuality, and class by making temporality appear as if leading inevitably toward national or communal unity. This is the case in *People of the Raven* as well as in the news stories about Michelle and Barack Obama's genetic ancestry. It is noteworthy that the newspaper articles operationalize evolutionary nostalgia when discussing historical (rather than prehistoric) events by insisting on the epistemic primacy of genetic knowledge. I have also argued that the smooth operation of population genetic temporality in general, and evolutionary nostalgia in particular, is complicated by the ways in which alternative temporalities may rupture the progressive push of evolutionary narrative. This may take place through cyclical, halted, or reversed time, as in *The Peppered Moth*, or through the idea of DNA as unfolding differently in different situations, as in the two articles on the Obamas's unexpected ancestry. This simultaneous presence of certainty (seemingly inevitable forward movement of time) and ambiguity (alternative temporalities, unfolding differences) is a key reason why population genetic discourse has proven popular as a source of imagining roots, destinies, and belonging. With slight twists of the temporal-affective dynamic underlying population genetics, a range of mutually contradictory accounts of communal boundaries and origins can be engendered and reinforced.

The mutability of DNA as a cultural symbol contributes to the remarkable flexibility of population genetics as a source for enacting personal, communal, as well as national forms of belonging. As my analysis

of *The Peppered Moth* and the two newspaper articles suggest, DNA carries a host of cultural and social meanings that erase its scientific meaning and function. As *The Peppered Moth* indicates, the cultural figure of DNA is able to invoke various scientific and nonscientific imaginaries and vocabularies, so that the considerable methodological and theoretical differences between population genetics and other forms of genetics disappear from the view. This flexibility makes genetic discourse affectively appealing, as it provides a logic of association through which the idea of prehistoric evolutionary origins and the idea of inherited behavioral and physical characteristics can be invoked simultaneously in a seemingly effortless manner. For example, the way in which mtDNA comes to stand for behavioral patterns in *The Peppered Moth* is an illuminating example of the rhetorical flexibility of genetic discourse. Furthermore, genetic discourse gives rhetorical force also to accounts of belonging that do not explicitly mention genetics. As my analysis of *People of the Raven* suggests, the central temporal dynamic of the novel—what I have called evolutionary nostalgia—resonates with popular discourses of manipulation and cloning of genetic material. In other words, while the novel does not discuss genetics, its use of evolutionary nostalgia echoes the idea that genetic sequences can be revised so that a new, better present and future will appear. These affinities between nongenetic and genetic imaginaries suggest that population genetic temporalities operate as a rhetorical and affective resource in culture also beyond genetic discourse.

This ability of DNA to cross discursive boundaries and to bring together various cultural vocabularies renders it a significant tool of collective memory. It is prosthetic in the sense that it engenders connections between individuals and imagined communities across time and space in notably flexible ways. This results in the extension of the reach of the affective present to the prehistoric past. The past becomes engulfed within the search for roots and belonging originating in the social, political, and cultural concerns of the present. Moreover, the very idea of turning to the distant past in the first place is a project motivated by the interests of the present. Collective memory provides one of the vocabularies through which the evolutionary past is turned into a culturally resonant affective

resource. The widely circulating idea of DNA as witnessing and remembering the past renders the affective ties between the past, present, and future mechanisms of remembrance and recollection. At the same time, the ambivalent nature of DNA as personal and unique yet abstract and shared complicates the idea of memory as collective. This becomes evident in the articles on the Obamas. While both articles invoke ideas of personal, communal, as well as national ancestry and the need to remember the complicated racialized past, neither study had access to the Obamas' DNA, nor did the Obamas provide background information or comment on the findings. So whose "personal" belonging do the articles construct then? What is the relationship between this configuration of belonging and the communal and national practices of recollection and remembrance? The prosthetic nature of DNA as an arbiter between the unique and the abstract masks some of these tensions in the two articles. Yet, as my reading of *The Peppered Moth* suggests, there are always moments of temporal interruption that make visible the uneasy coexistence and underlying incommensurability of personal, communal, and national forms of evolutionary belonging.

In the next chapter, I return to the question of the affective present as the ultimate origins of belonging. I explore how the politics in the present defines the search for roots and destinies. I focus on the idea of community that emerges in visions of the present and future as rooted in the evolutionary past. In particular, I ask how the interplay between sameness and differences so central to population genetic practices informs the ways in which population genetics is mobilized to construct contemporary communities as exclusionary or inclusionary.

Notes

1. Feminist scholars in particular have critiqued narratives that bring together two mutually complementary lovers and thus mask the ideological tensions the narrative may have raised. For classic critiques, see Rachel Blau DuPlessis (1985) or Teresa de Lauretis (1984). See also Roof (1996), Pearce and Stacey (1995), or my article (Oikkonen 2010).

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5

Genetic Communities and the Boundaries of Belonging

With the rise of popular genetic discourse during the Human Genome Project (1990–2003), an increasing number of social networks and communities have emerged around genetic knowledge. While there is nothing new about people with shared interest, such as personal experiences of a given illness, seeking out each other, the genetically framed forms of social organization posit molecular variation within our cells as a key constituent of belonging and identity. These new forms of social organization have received considerable attention by researchers working within sociology of health, social, and cultural anthropology, and science and technology studies. Central to this research has been the concept of *biosociality* coined by anthropologist Paul Rabinow (1996) and developed further by many others (e.g. Gibbon and Novas 2008; Rose and Novas 2007). Biosociality refers to the ways in which communities, identities, and affiliations emerge around biomedical knowledge about individualized biology, such as genetic variation or susceptibility to particular diseases.

In his 1996 exploration of biosociality, Rabinow famously predicted that biosociality will emerge even around minute genetic mutations. Indeed, today, communities of patients and their relatives often operationalize scientific studies on the genetic basis of specific conditions to

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strengthen the ties between members of the community, to lobby for research funding, or to advocate for better services. Sometimes the role of genetics is pivotal: since Huntington's disease is caused by a genetic mutation with dominant inheritance, genetics is an integral part of Huntington's communities (Novas and Rose 2000). In many other cases, the genetic connection is more tentative or marginal: for example, Daniel Navon and Gil Eyal (2014) show how biosocial practices appear around a proposed connection between a rare genetic disorder and autism. However, the role of genetic factors in inherited conditions does not mean that biosocial communities simply embrace biomedical research. Although certain forms of hearing impairment or short stature (dwarfism) have a genetic basis, communities around these conditions engage in critique of ableist norms about the primacy of hearing or assumptions of normal height.

While biosocial communities and practices built around medical conditions have engendered many scholarly analyses, less attention has been paid to nonmedical genetic knowledge. In this chapter, I examine how genetic information that does not have direct medical value becomes part of the rhetorical resources through which communities are built, strengthened, and reoriented. In particular, I ask how population genetic technologies become means of making and shaping communities. Alondra Nelson (2016) has produced insightful ethnographic work on how African-American communities embrace and mobilize genetic ancestry research to establish roots in African countries or regions, to strengthen African-American communities in the present, to make legal claims based on ancestry, and to provide affective resources for personal identity work. While inspired by this line of research, my focus is different: rather than asking how population genetics is invoked and operationalized in specific communities, I explore how population genetics becomes seen as a means of enacting various, mutually incompatible communities. My focus, that is, is not on biosociality as a phenomenon, but on the technological, material, epistemic, and cultural *preconditions* through which population genetics comes to be seen as a ground for biosociality and communal belonging.

The chapter elaborates on several themes developed in the previous chapters. First, it explores the ways in which the idea of community grounded in population genetic models relies on specific technological

practices of mitochondrial DNA (mtDNA), Y-chromosome, or genome-wide analyses, and how these practices enact communities in different ways. There is no single model of community arising from population genetics. Instead, there exist multiple models of community that are inseparable from the logics of knowledge production and the methods of making differences and sameness that produce them in the first place. Second, the chapter elaborates on how the availability and selection of biological material and reference sequences affect what kinds of communities emerge as believable or desirable. The material circumstances of knowledge production within and around population genetics thus not only shape genetic ties—a central theme of the previous chapters—but also structures how those ties engender communities. Third, the chapter picks up the theme of temporal distance as producing sameness and difference introduced in the previous chapters. It examines how different techniques, technologies, and research questions engender an array of comparisons across time and space, and how those comparisons generate changing constellations of difference and sameness. These patterns of difference and sameness, in turn, make up the very fabric out of which communal boundaries—understood both temporally and geographically—are crafted.

The chapter builds on the conceptual framework developed throughout the preceding chapters. I continue to draw on the idea of population genetic technologies and practices as affectively charged. This affective underpinning of technologies and practices renders them powerful resources for a diverse set of projects of communal belonging. For example, the mobilization of temporal distance in invocations of genetic community cannot be separated from the affective temporal structures such as evolutionary nostalgia that root the community within a dynamic of longing that sees the past as a source of futurity. I also highlight both resonances and tensions between different kinds of population genetic communities. I show how these resonances and tensions arise from the ultimate ambiguity of genetic material as a source of knowledge about the webs of relations through which we belong. Furthermore, following the main argument of the book, I propose that the tensions and resonances between the multiple and largely incommensurable communities that arise around population genetics are what makes population genetics so

appealing as a resource for imagining belonging. This is the crux of the argument: population genetics is flexible as an affective resource in that it can be mobilized to support multiple communities; yet the material conditions of population genetic knowledge production—techniques, samples, methods, practices—shape those communal projects in fundamental ways, setting the limits of how communities can be enacted. The interplay of these two tendencies results in population genetic communities being premised on irresolvable tensions.

The chapter begins with a discussion of the relationship between the key concept of population genetics—*population*—and the cultural concept of *community*. I explore how population operates as a remarkably flexible analytical tool in population genetics, and how this analytical and situated use of the concept is in tension with the affectively charged idea of community. I suggest that the tension between population and community in fact strengthens the appeal of population genetics by invoking diverse cultural imaginaries and multiple affective resonances. After laying out this tension, I turn to two phenomena that highlight how the making of population genetic communities mobilizes inclusions and exclusions. First, I explore the search for sameness across evolutionary time in direct-to-consumer genetic ancestry tests. I investigate how these commercial technologies enact several kinds of population genetic communities—most importantly, dichotomously gendered communities—and how such communities are inseparable from the modes of analysis chosen by the companies. I also show how the search for likeness that motivates the tests is produced through an underlying logic of difference. My second focus is on the dynamics of exclusion in how population genetic knowledge is invoked in the search for genetic "Europeanness," on the one hand, and national belonging within Europe, on the other—two projects that are often in tension. I approach these issues through the case of Finland and the idea of "Finnish" genetic inheritance. Furthermore, I examine how population genetics becomes mobilized in current public debates about migration and multiculturalism in Europe and in Finland, and how the idea of genetic community can be invoked to support both progressive and reactionary politics. The chapter concludes with a discussion of the political implications of the idea of population genetic

community, and especially the discrepancy between the concept of population and the idea of community.

Population and Community

Science studies scholars have analyzed the concept of *population* in various practices that have emerged within and around human population genetics. One strand of research has focused on the uses of population in lab practices. This research has highlighted the flexibility of population as an analytical concept. For example, Amade M'charek (2005, 21–55) shows how population can be used in several different ways within the same research setting, such as the study of forensic DNA collected as part of criminal investigation, to tease out patterns of difference and sameness between a DNA sample and reference DNA. Such uses of population as an analytical tool are usually motivated by specific research questions: in the case analyzed by M'charek, to connect a sample from the crime scene to genetic variation among populations. M'charek notes "that geneticists cannot know the individual without a population" and "that in genetics neither the individual nor the population are inherently 'biological.' Rather, they are effects of technologies and routines applied in scientific practice" (M'charek 2005, 21).

M'charek's observations resonate with Deborah Bolnick's (2008) analysis of how computer software used in the analysis of sequenced samples produces populations. For example, a researcher can program software to identity a certain number of clusters (closely related samples), which then generates a particular web of genetic ties and a particular dynamic of sameness and difference. Likewise, programs draw on different statistical models, which enact different sets of populations. Populations, then, are not natural objects but products of technoscientific practices. This becomes also evident in Joan H. Fujimura, Ramya Rajagopalan, Pilar N. Ossorio, and Kjell A. Doksum's analysis (2010) of how two current genomic approaches to genetic variation—admixture studies and genome-wide association studies—mobilize and reinforce different conceptions of population. What counts as a population in different situations is inseparable from the chosen analytical approach, methodological

decisions, technological development, statistical models, research questions, and routinized lab practices (see also Hinterberger 2012b).

Science studies scholars have also highlighted the ways in which the concept of population is shaped by scientific and cultural histories. Jenny Reardon (2005, 2008) shows how the concept of population is haunted by the unclear connection between population and race. While population geneticists often emphasize that population is a technical term that does not indicate racialized essence, the way in which populations often coincide with cultural ideas of races—for example, the assumption that Africans, Native Americans, or Europeans constitute clearly defined groups—has raised questions about what exactly is the difference between population and race. Indeed, Lundy Braun and Evelynn Hammonds (2012) demonstrate how classic population genetic studies draw on much older anthropological categories of racialized groups in Africa.

Historical and cultural developments also impact how populations are conceptualized in scientific projects. For example, biomedical research into population differences often utilizes census information. As censuses operate within national frameworks and mobilize varying sets of historically formed population categories, the population information derived from a census reflects national or local cultural histories rather than any scientific definition of population (Hinterberger 2012a). The use of census information also highlights another dilemma: the role of self-reporting of ancestry. Despite recognized problems with self-reporting, such as people identifying with ethnic background in multiple and contradicting ways, many research projects still utilize ethnic self-identification (Tutton et al. 2010). Furthermore, church records and other local archives are used as a source for constructing genetic family ties in research on genetic variation within populations. Anthropologist Nina Kohli-Laven (2012) demonstrates how this leads researchers working on rare inherited diseases among French-speaking families in Quebec, Canada, to make assumptions about family ties that are simply not true. For example, the practice of giving a French name to indigenous people who converted to Catholicism and married a French colonist disguises the reproductive connections between indigenous people and colonists. This leads to the misleading appearance of the French-speaking people in Quebec as a genetically homogenous population.

Several scholars (e.g. Hinterberger 2012a; Tutton et al. 2010) point out that these diverse uses and definitions of population are brought together through what Steven Epstein (2007) has called *categorical alignment*. That is, incompatibilities between these uses and definitions of population are erased though their inclusion within the framework of genetic research. As a result, categories become aligned so that they no longer appear incompatible. Nevertheless, tensions remain. This becomes visible, for example, in the construction and justification of biobanks, the systematic collection of biological material and health information from a particular local, ethnic, biosocial, or national population. Aaro Tupasela, Karoliina Snell, and Jose Cañada (2015) argue that biobanks attain their legitimacy and perceived uniqueness through the idea of a distinct population that they source and archive. At the same time, biobanks need to constantly construct that population as unique and clearly defined. Tupasela and colleagues describe this relationship between population and biobank as one of co-construction. In this dynamic, the uniqueness and coherence of a population is a product of repetition and ongoing discursive and epistemic work. Such work involves maintaining the alignment of social, cultural, historical, and scientific definitions of population that enabled the construction of the coherent source population in the first place.

The idea of *community* both resonates with and differs from population in crucial ways. Compared to the technoscientific clang of population, community is clearly embedded within ideas of social organization and cultural belonging. A useful starting point for understanding community is historian Benedict Anderson's ([1983] 2006) famous conceptualization of communities as *imagined communities*. Focusing on the idea of national community and the emergence of nationalism, Anderson asks how people who cannot all know one another become committed to the idea of a coherent national entity of people motivated by a shared national purpose. It is noteworthy that this dilemma of not knowing your fellow members of the community also underlies genetically framed communities, where the revelation of a genetic connection or similarity is often the only tie that initially connects people; this is the case, for example, with genetic ancestry tests analyzed in the following sections.

Another characteristic of community is the simultaneous existence of multiple communities within a person's life. Ethnic, familial, regional, or national communities do not necessarily exclude one another, even if one takes presence over others in particular situations. However, there are often tensions between these forms of communal belonging, as my analysis of the personal, regional, and national forms of belonging in the media coverage of Cheddar Man suggested. Yet another feature of community is the underlying assumption that communities and communality encompass a range of social, cultural, and psychological ties. This means that whatever the initial basis of community—shared genetic markers at particular genomic loci, for example—communities are perceived as engaging us in the full affective and embodied experience of belonging. Social, cultural, and psychological dimensions are brought together through the organizing assumption of a shared sense of purpose. Such a purpose may arise from shared experiences, as in the case of shared genetic markers discussed in the following sections, or it might be more openly political, as in some of the invocations of a homogenous national community discussed at the end of the chapter.

Communities, like populations, need to be constantly maintained and reproduced. Like populations, communities are not natural, coherent entities. Priscilla Wald's (2008) study of the outbreak narrative—the narrative of the emergence and eventual containment of a life-threatening infectious disease—provides an illuminating example of how communities are constantly constructed. Tracing the appearance and variations of the outbreak narrative through twentieth-century American history, Wald shows how the idea of national community—conceptualized in terms of white, Anglo-American, middle-class interests—takes place through constant negotiations over physical boundaries (the prevention of contacts that might help epidemics cross borders) as well as symbolic boundaries reflecting gendered, sexualized, racialized, or classed hierarchies that separate people. This ongoing maintenance work makes communities appear as rooted in history and as moving steadily through the present toward futurity.

Both population and community often invoke more than they are "technically" supposed to mean. Although population is primarily an analytical concept in lab practice and computer modeling, its unclear

relationship to race enables a range of cultural imaginaries of racialized difference and belonging to emerge around it. Likewise, in cultural discourses of community there is often an implicit or vaguely articulated assumption of a biological foundation, that is, an assumption that in the heart of community is something more fixed and timeless than culture and society. This suggests that population and community are mutually entangled concepts. Contemporary invocations of genetic discourse in order to build or consolidate communities, then, are not really new. Rather, they articulate and enact an existing entanglement of two ideas—population and community—in novel ways.

The rhetorical appeal of population genetic discourse as a means of building communities arises from these resonances, tensions, and entanglements. The population genetic framework makes it possible to root communities in evolutionary history beyond the historical record, as I argued in the last two chapters. The genetic framework also posits genetics as a symbol of permanence and unambiguity, and thus as a guarantee of communal continuity and futurity. This is, of course, ironic considering the flexibility and ambiguity of population as a scientific concept. At the same time, the concept of population accrues growing cultural salience through its association with the affective, psychological, and sociocultural scope of communal belonging. In short, while communities gain epistemic authority and an ontological justification through the invocation of population genetic discourse and the widely recognized idea of DNA as ultimate evidence, genetic models of population become seen as increasingly significant through the myriad cultural associations underlying the idea of community.

In the sections that follow, I explore the simultaneous flexibility and fixity of population as a concept through which communities and communal belonging are being reimagined in contemporary culture. I am interested in the ways in which different conceptions of population enact different formations of community. While a number of scholars have investigated the many uses of population in scientific practice, there is little research on the cultural narratives and vocabularies through which the connection between population and community is imagined and maintained. This fragile yet persistent connection between population

and community is in the heart of the phenomena that this chapter addresses.

Commercial Genetic Ancestry Tests

The first commercial genetic ancestry tests appeared around the year 2000. Since then, the number of companies marketing tests directly to consumers has multiplied, and by today, over three million people have purchased genetic ancestry tests (Smart et al. 2017). There are currently over 20 biotechnology companies that sell genetic tests for the detection of "admixture," "deep ancestry," or "genealogy," though some of these companies are owned by other companies, or they buy services from each other (International Society of Genetic Genealogy Wiki 2017). The companies operate through online sites, where the prospective customers can order various test kits ranging from less than 100 US dollars to several hundred depending on the "resolution" of the test—that is, how many genetic markers are being tested. Once a test has been purchased, the company sends the customer a test kit and instructions for a cheek swab or a collection of saliva. The test kit is then sent back to the company, which delivers the results usually within two months. Results typically include a report on the genetic analysis conducted by the company, downloadable raw data, ancestry maps, certificates of ancestry, as well as access to an online interactive platform where the customer can search for new genetic "relatives," that is, other people who have bought a test from the same company and who share, for example, the same Y-chromosome haplogroup.

Commercial genetic ancestry tests have been approached as appealing tools for personal genealogy research, personal and communal identity projects, as well as practices of self-tracking. Genetic ancestry testing has been discussed widely on family genealogy forums, and one of the leading genealogy research companies, Ancestry.com, offers genetic tests in addition to archival tools for genealogical inquiry. While genetic ancestry tests are popular across the global north especially among the middle classes, the tests carry particular appeal among African Americans, as genetics is seen as a way of establishing roots in Africa beyond the

devastating history of slavery (Nelson 2016; Schramm 2012). Furthermore, much like wearable self-tracking devices, ancestry tests have appeared as means of turning our bodies into a source of personal, quantifiable data. In his overview of new constellations of race and genetics, sociologist David Skinner links the emergence of genetic ancestry testing "to changing values around consumption, personal development and individuality. Part of the appeal of these forms of genetic testing is the way that they appear to provide a means of reconciling increasingly individualized accounts of self-identity and the constitution of political communities in racialized form" (Skinner 2006, 482). All in all, it is noteworthy that people use the tests for a range of purposes that may differ from the uses the tests are marketed for (Ruckenstein 2016). Likewise, test-takers may combine the test results with personal narratives and cultural vocabularies in ways that clearly depart from the science of population genetics (Nelson 2016; Schramm 2012).

Since their appearance in the direct-to-consumer biotechnological market, genetic ancestry tests have received considerable criticism from bioethicists, legal scholars, and social scientists (Bolnick et al. 2007; Greely 2008; Lee et al. 2009; Schramm 2012; Wagner 2010). Criticism has centered on whether the knowledge genetic ancestry tests produce is actually epistemically valid and whether people buying tests are made aware of the limits of the results they are given. For example, reflecting the statistical underpinnings of population genetics, genetic ancestry tests are probabilistic: they provide an educated evaluation of the most likely model of ancestry for a specific sample. That evaluation, in turn, relies on the database of previously collected samples against which the tested sample is compared. As I have argued throughout the book, population genetic knowledge is relational in the sense that the uniqueness of a given sample arises only through its comparison to other samples or to reference sequences (such as the mitochondrial reference genome sequenced in 1981). Genetic testing companies vary, however, in what kind of a database they have available for the analysis. The database typically consists of a growing collection of samples retrieved from previous customers, and may include selected publically available sources on genetic diversity. The relationality of genetic ancestry also means that the geographical and ethnic background of customers matters: if the database

consists primarily of samples collected from Europe, an African-American customer is unlikely to receive detailed results—and vice versa. As the companies' own databases are usually proprietary, the results cannot be compared to the databases collected by other companies. The results of the tests also depend on the genetic loci selected for analysis. As companies test for different sets of markers, a person buying ancestry tests from several companies may receive somewhat different results from each test.

While ethical and social questions surrounding genetic ancestry tests are important, I will focus on the ways in which genetic ancestry tests emerge as affectively and rhetorically appealing means of enacting community. However, instead of studying test-takers' ways of using ancestry tests to build community, I explore the preconditions of the idea of population genetic community. I am interested in genetic ancestry tests as part of the larger phenomenon of reimaging belonging through population genetic technologies. Following the argument of the previous chapters, I investigate how the specific technological practices used by these companies reinforce specific forms of community. My analysis traces differences between the communities produced through mitochondrial, Y-chromosome, and genome-wide techniques. I also ask how evolutionary distance engenders different types of communities, and how boundaries of communities are produced through acts of mapping.

Gendered Communities

In her book *Genetic Geographies*, Catherine Nash argues that "[h]uman population genetics is as much about sex as it is about race, ethnicity, or nation. It is about multiple instances of who has sex with whom or, to put it more scientifically, how their specific and cumulative reproductive outcomes shape individual ancestries and patterns of genetic variation" (Nash 2015, 137). Nash shows how mitochondrial and Y-chromosome lineages traced by population geneticists have become increasingly entangled with cultural ideas of complementary masculinity and femininity, such as narratives of male promiscuity and prowess, gendered division of labor, and distinct male and female human natures. This invoked dynamic of sexual difference is mapped on prehistoric continents as strictly

gendered patterns of migration, as if men and women followed largely different evolutionary paths. My reading of genetic ancestry tests echoes Nash's observation in many ways. I highlight how the tests produce gendered forms of belonging, and how the gendering of belonging comes to define the ways in which communal boundaries are imagined. Elaborating on the idea of evolutionary nostalgia developed in the previous chapter, I suggest that genetic ancestry tests operationalize nostalgic longing for gendered communal futures.

Companies selling commercial genetic ancestry tests typically provide three main types of tests: mitochondrial analysis, Y-chromosome analysis, and admixture analysis. Mitochondrial and Y-chromosome tests seek to establish a link between the tested sample and a specific, geographically located mitochondrial or Y-chromosome haplogroup in the evolutionary past. Admixture tests, by contrast, estimate the percentage of DNA across the genome that the customer shares with populations such as Native Americans, Europeans, or East Africans. All of the tests rely on a selection of the so-called ancestry informative markers or other molecular loci considered to represent variation between populations. The selection of markers is crucial for producing relatedness. In general, the bigger the number of loci tested, the more detailed the results—although, as explained above, the size and constitution of the database play a key role as well.

Mitochondrial, Y-chromosome, and admixture tests differ in their temporal investments. Mitochondrial and Y-chromosome tests produce a temporal trajectory from a specific site in the present to what is imagined to be a specific location at a particular historical moment in the prehistoric past. Admixture tests, in turn, focus on the present by highlighting the outcome of evolutionary processes—the interconnections among modern humans—rather than their roots. The trajectories that mitochondrial and Y-chromosome tests generate are strictly gendered, representing exclusively matrilineal and patrilineal reproductive connections. As I suggested in the context of Mitochondrial Eve and Y-Chromosome Adam in Chap. 2, such a focus on uniparental inheritance erases the complex web of genetic relatedness that connects us to the evolutionary past. That is, reproduction appears as a specific mode of heterosexual reproduction in which generations are connected through the passing of a largely unchanged set of genetic markers along strictly gendered lines.

This results in a curious coexistence of parallel temporalities: a matrilineal evolutionary temporality and a patrilineal one. What makes this assumed parallelism of mitochondrial and Y-chromosome ancestry particularly curious, as Nash (2015, 137–169) points out, is that only Y-chromosome analysis traces gender-specific genes. Although only women pass mtDNA to their children, we all carry mtDNA in our cells, and there is no direct connection between mitochondria and gendered physical or behavioral characteristics.[1] As to admixture tests, compared to mitochondrial and Y-chromosome tests they appear as largely nongendered, representing a range of markers across the genome inherited from all of our parents, grandparents, great-grandparents, and so on. Yet admixture tests, too, rely on an implicit heteronormative dynamic in which reproductive success—the production of offspring who in turn produce offspring—emerges as the ultimate tie between the past, present, and future. However, I focus here on mitochondrial and Y-chromosome tests, as they illuminate the gendered underpinnings of genetic communities in particularly interesting ways.

The temporal investments of genetic ancestry tests become visible in the way in which testing companies frame them as providing unprecedented access to the past, and, through that past, to a new vision of the present. This framing is, however, inherently contradictory. The companies' websites typically produce a sense of a unified evolutionary past that we all (should) desire to access. An illustrative example is the website of Roots for Real, the company involved in the 2003 BBC documentary *Motherland: A Genetic Journey*, which traced the genetic roots of members of the African diaspora in the United Kingdom. The Roots for Real website portrays genetic ancestry as an implicitly unified field and contrasts it with traditional genealogy: "Most of us can trace our family history for a few generations—possibly down to our great-great-grandparents—but certainly not thousands of years into the distant past, when Europe and other continents were settled by prehistoric tribes and peoples" (Roots for Real 2017a). We are told that "[i]n the genetic material in each of us, a mass of historic information is encoded, with which experts can for the first time gain clues to our past ancestors" (Roots for Real 2017a). This vision of the genetic material in our cells as "mass of historic information"

produces a sense of the evolutionary past as a single, uniform site that can be accessed in a straightforward manner through the tests. Similarly, an introductory video on the commercial genetic testing site called DNA Ancestry Project frames the tests it sells in the following way: "Trace your roots… Unearth your ancestry… Discover your family story… Become a part of history" (DNA Ancestry Project 2017). While the video posits genetic testing as an extension and improvement of traditional genealogy, it also invokes human evolutionary history as a monolithic and irresistible temporal push from the prehistoric past to the present and toward future. The video urges us to "become a part of history" by joining the totalizing movement of evolutionary time toward futurity as if we were not part of historical processes prior to the knowledge produced through genetic tests.

The assumption of a uniform, totalizing passage of history recorded in our genetic material is in tension with the idea that specific tests unfold distinct temporal trajectories between us and our unique evolutionary roots. The testing companies often highlight the specificity of the connection to the past provided by different types of tests. For example, Oxford Ancestors, one of the oldest ancestry testing companies operating from the United Kingdom, dedicates a separate page for "maternal ancestry" and "paternal ancestry." The maternal ancestry page explains that the "MatriLine™ service" compares the "precise sequence" of the customer to "the many thousands of others from all over the world that we have in our database" in order to identify "to which of the clans you belong, and from which ancestral mother you are descended" (Oxford Ancestors 2017b). Moreover, the page highlights the linearity of the gendered temporal connection: "Everyone in the same clan is a direct maternal descendant of one of these clan mothers and carries her DNA within every cell of their body. Your mtDNA actually helps cells use oxygen—so you are using your clan mother's mtDNA every time you breathe" (Oxford Ancestors 2017b). Interestingly, this last sentence not only genders the linear temporal trajectory the test produces but also posits the discovered gendered past as the precondition of the test-taker's embodied existence in the present and future. The paternal ancestry page uses similar rhetoric, emphasizing how "our classic Y-Clan service" is able to trace "your

paternal clan and your ancient ancestral father" and to "give you some information as to when and where he lived" (Oxford Ancestors 2017c).

Word choices such as "ancestral clans" and "clan mother" and "ancestral father" further imply that the past discovered through genetic tests is specific in the sense that it materializes in a single prehistoric man or woman, rather than, for example, the frequency of a particular haplogroup across geographically diverse populations. On Oxford Ancestors' website, this claimed specificity is emphasized through the act of giving classical and symbolically charged names, such as Tara, Helena, and Xenia, to the imagined prehistoric "clan mothers" representing European mitochondrial haplogroups (Oxford Ancestors 2017b). The perceived specificity of Y-chromosome results is highlighted in turn by some companies' promise to provide information on whether the male customer is related to famous historical men. For example, Roots for Real aims to "inform you whether your Y-type matches the Jewish Cohanim Y chromosome (thought to be the Y chromosome of Moses and his brother Aaron), or the Y-types of Genghis Khan, President Jefferson and other historic personalities" (Roots for Real 2017c).[2]

While testing companies' rhetoric celebrates "deep" roots as the true location of belonging, the tests are nevertheless primarily concerned with the present. The present is the affective temporal site at which identities, connections, and boundaries are being negotiated and enacted through the very decision of purchasing a genetic ancestry test, or adding one's results to an interactive customer platform in order to discover genetic relatives. This primacy of the affective present becomes evident in ethnographic studies of how people use genetic ancestry tests in their private and social lives (see especially Nelson 2016). My interest lies, however, in how the gendered trajectories produced through the testing technologies shape the *idea* of community and communal belonging in the present. The concept of evolutionary nostalgia developed in the previous chapter provides an elucidating lens into this dynamic. As I argued through my reading of *People of the Raven* and the media stories of Michelle and Barack Obama's genetic ancestry, evolutionary nostalgia mobilizes a sense of longing toward the previously unknown past in order to enact an alternative and better present and future. This temporal dynamic also organizes genetic ancestry tests. First, the tests are typically depicted by the

companies as generating unexpected results. For example, Oxford Ancestors highlights the "element of wonder" that accompanies the ability of genetics to reveal "the elegant simplicity" of our roots in thrilling and unexpected ways (Oxford Ancestors 2017a). Similarly, Ancestry.com promises to make the prospective customer "[c]onnect with relatives you never knew you had," and showcases the story of a woman from New York City with roots in Colombia whose "DNA results took her ancestry to unexpected places" beyond the regions she expected (Ancestry.com 2017).[3] Second, the unexpected new genetic "relatives" and webs of relatedness that the tests enact in the present are often portrayed as the ultimate community that one belongs to. The longing to establish roots in the prehistoric past that justified the tests in the first place thus results in the production of a new genetic community and new forms of communality in the present. While the preexisting and soon-to-be-discovered communities often intersect (e.g. in the case of close family relations), the cultural prestige of DNA as a symbol of ultimate belonging encourages privileging the patterns of relatedness produced through genetic tests. Moreover, the celebratory tone of genetic ancestry testing websites suggests that these new, unforeseen communities should be viewed as a gateway to a more enlightened and emotionally fulfilling future. As with the texts read in the previous chapter, the evolutionary past comes to stand for a promise of futurity and continuity.

In the rhetoric of genetic ancestry testing, then, the existing social network of relations within which the prospective customer currently lives becomes supplemented or even supplanted by a previously *invisible* community that is rendered *visible* through the practice of genetic testing. However, it is in fact the act of genetic testing that brings that community into existence in the first place. At the same time, this new community appears as the connection between the existing present and a better future. This is what happened in the *New Your Times* article on Michelle Obama's ancestry in the previous chapter: genetic testing was seen as *revealing* family ties between the descendants of white slave owners and black slaves, while the act of testing actually *constituted* those ties as more material and incontestable than the cultural and emotional ties within each family. At the same time, the interracial ties enacted through genetic testing emerged as a novel, firm ground for reaching toward a harmonious

multiracial future. Where the marketing of mitochondrial and Y-chromosome tests differ from the narratives explored in the previous chapter is in their gendering of the new genetic communal presents and futures enacted through the tests. The assumption that mitochondrial and Y-chromosome lineages constitute parallel, gendered trajectories renders the to-be-discovered genetic communities in the present as symbolically gendered. As these gendered communities are positioned as epistemically primary to existing emotional and social ties, they come to be seen as the foundation of new gendered sociality. For example, when customers receive Y-chromosome DNA results, they are typically encouraged to search for other men with the same Y-haplogroup across the world through the company's interactive online platform and customer database. Intriguingly, these are precisely the kinds of gendered communities built around a single mutation or set of mutations envisioned by Greg Egan in the 1990s in the dystopic short story "Mitochondrial Eve" discussed in Chap. 2.

All in all, I would argue, the appeal of mitochondrial and Y-chromosome ancestry tests arises from this conjoiner of evolutionary nostalgia, gendering of belonging, and the symbolic resonance of genetic discourse. Evolutionary nostalgia invests the search for an imagined evolutionary past with a future-oriented temporal push. The material and technological practices of mitochondrial and Y-chromosome analyses render this search structurally gendered. As a result, the linear evolutionary trajectories constructed through the mitochondrial and Y-chromosome tests appear as ontologically separate, as if they represented two distinct ways of being and becoming. While mitochondrial analysis is not technically gendered in the same sense as Y-chromosome inheritance, the temporal pull of evolutionary nostalgia and the symbolic power of DNA as ultimate evidence erase these differences. Thus, the new genetic communities in the present that are enacted through the tests appear as gendered as well. Furthermore, the assumption of linear continuity and reproductive purity—the reproduction of specific haplotypes through generations—gives the emerging population genetic communities a sense of permanence and futurity. Crucially, this inherent potential for optimism is what might be missing from the existing communities within which prospective customers live.

Temporal Distance, and the Making and Unmaking of Communal Boundaries

I argued in the previous chapter that genetic knowledge relies on an underlying ambivalence about the materiality of DNA samples and DNA as an abstraction. I also suggested that this ambivalence is productive in that it invests DNA with remarkable epistemic authority: it enables the appearance of genetic material as a reliable historical witness to the scenes of the prehistoric tundra, and, at the same time, an endlessly malleable virtual code from which various potential futures may be crafted. In genetic ancestry tests, this ambiguity manifests itself in the insistence on the materiality and thus irrefutability of the test results, on the on hand, and the flexibility with which population genetics can be brought to enact various forms of community, on the other. In other words, while the tests are marketed through the rhetoric of precision, it is precisely the absence of precision that makes them appealing as a resource for imagining genetic communities. This becomes visible, for example, on the Roots for Real website, which includes a long list of different types of genetic roots their customers might search for through genetic ancestry tests, such as Native American, European, African-American, British African Caribbean, and Jewish ancestry (Roots for Real 2017c). These are neither ontologically symmetrical communities nor necessarily mutually exclusive, as they are positioned differently within the temporal dynamics of global human diaspora. Similarly, one of the major players in commercial genetic ancestry testing, Family Tree DNA, provides customers with an opportunity to establish and participate in local ancestry "projects" (Family Tree DNA 2017). Some of the projects are focused on the genetic roots of people from a specific town or region within a nation, or from areas encompassing several modern nations (the Baltic region, for example); some others attempt to establish genetic diasporas by inviting, for instance, people of Irish background living in a given US state to submit their test results for comparison. The sheer range of Family Tree DNA "projects" demonstrates that population genetic community can be defined at different levels of specificity.

Temporal distance is central in making population genetic communities. Depending on how far back we look in human evolution, different constellations of difference and sameness arise. In population genetics, sameness and difference are inseparable—sameness emerges only through its difference from something else, and difference appears through comparison to what is defined as likeness. For example, while genetic ancestry tests seek for new forms of likeness by identifying genetic relatives across the globe, that sameness relies on not being related to someone else. As Amade M'charek (2005) shows, the ways in which population genetics makes sameness and difference are flexible and situated. The adjustment of temporality is an important way in which difference and sameness are made: by zooming in or zooming out, different patterns of sameness and difference emerge. This temporal flexibility enables the invocation of population genetic community simultaneously at multiple levels—regional, continental, global—in genetic ancestry tests.

The temporal ambivalence renders population genetic communities remarkably porous. This becomes visible in the practices of mapping that underlie and result from population genetic research. Maps and mapping constitute a powerful metaphor in population genetics. Mapping can simply refer to the sequencing of previously unknown genetic material, for example, the idea of "mapping the genome" in the context of the Human Genome Project. But maps and mapping have also other uses and meanings. Population genetics maps human genetic variation into webs of relatedness, such as visual illustrations or diagrams of *genetic distance* between different mitochondrial or Y-chromosome haplogroups. In such maps, the temporal element may be downplayed, as the "map" reflects the present stage of genetic variation. Population genetics also produces prehistoric migration maps, in which patterns of human mobility are represented through arrows leading, say, from an older mitochondrial haplogroup located in eastern Africa to a newer haplogroup that arose from it in the Middle East after the first anatomically modern humans left Africa. In such maps, the idea of difference produced through temporality—the appearance of a mutation that leads to the emergence of a new mitochondrial haplogroup—is mapped onto global geography as patterns of prehistoric migration. Some other population genetic maps operationalize geography through a similar image of continents, but this

time the continents and the haplogroups listed on the map reflect the current distribution of genetic variation across the globe—for example, showing the most common haplogroup in each region—rather than evolutionary movement.

Furthermore, some genetic maps demonstrate genetic relatedness of populations through sets of dots representing populations. While some sets of dots are relatively uniform, suggesting genetic homogeneity within the population, others may be more dispersed, indicating heterogeneity within the population. Sometimes these dots follow the patterns of recognizable geographical contours and national borders (see, for example, Novembre et al. 2008).[4] Yet such a map is a map only in metaphorical sense: the distance between individual dots or between sets of dots measure genetic difference instead of geographic distance. This type of map can be produced around specific molecular loci, a specific sequence, or even the overall of the genome.

Commercial genetic ancestry tests use several of these maps. For example, Roots for Real has a page dedicated to "Ancient Migration" with a slide show that demonstrates the emergence of mitochondrial haplogroups through human evolution spanning from the original haplogroup of Mitochodrial Eve in "South or East Africa about 150,000 years ago," to how "60,000–30,000 years ago, humans gained tenuous footholds in the continents of the Old World," to how "[a] small group of Homo sapiens from northern Siberia moved into the Americas" some 25,000 years ago, and eventually to "the peopling of Madagascar (1500 years ago) and the Pacific (mostly 1000 years ago) by seafaring Austronesians" (Roots for Real 2017b). The 12 slides consist of a changing set of arrows and circled letters placed on the world map: circles in pale green represent old mitochondrial haplogroups, circles in bright yellow represent emerging haplogroups, and arrows indicate the migration of populations that result in the emergence of the new haplogroups and their gradual spread across the continents. The slides highlight movement and patterns of continuity from the prehistoric Africa to the modern world.

At the same time, "Our services" page on the website provides an example of the kind of personalized maps that customers purchasing a Y-chromosome or mitochondrial test will receive. These products are

framed as "totally individual … showing where in the world you have matches, to estimate the location of your ancestral origins" (Roots for Real 2017c). The sample mtDNA maps indicate with colors the areas in the world where the test-takers' mtDNA haplogroup represents more than 0%, more than 3%, and more than 10% of mitochondrial samples from that area. The sample Y-chromosome map gives the same visual information for areas where the tested Y-chromosome haplogroup matches more than 0%, more than 1%, and more than 3% of Y-chromosome samples from that area. In addition, the sample Y-chromosome map locates a "geographic center" for the customer's Y-chromosome haplogroup. The sense of movement and unstoppable passage of time that underlies the Roots for Real slide show is absent in these personalized maps. Instead, the personalized maps suggest the existence of a new genetic community built on the current global spread of a specific mitochondrial or Y-chromosome haplogroup.

These are just two examples of the kinds of mapping practices that ancestry testing companies craft and mobilize. Most companies seek to establish their own unique (often trademarked) maps that are represented as generating a truly unique experience. These practices of mapping produce a sense of concreteness and precision, as if the maps as material objects provided a concrete foundation on which to build one's identity and genetically grounded forms of community. Yet, the heterogeneity of mapping practices and ways of visualizing difference and sameness show that the rhetoric of precision in which the maps are embedded is illusionary. The mobile view of the emergence of mitochondrial haplogroups through spatial and temporal movement in the Roots for Real slide show is in clear tension with the stable view of genetic difference indicated by the personalized mtDNA and Y-chromosome maps on the same website. While the visual rhetoric of arrows and numbers in the slide show seeks to capture the temporal and spatial dynamic through which variation is produced,[5] the personalized maps attempt to establish an ontology of belonging rooted in stability and permanence. Depending on the way in which we visualize and map genetic difference and sameness, the boundaries of genetic communities look very different. Yet these considerable tensions do not seem to diminish the cultural resonance of population genetic maps as means of

enacting genetic communities—quite the contrary, they provide a range of visual tools that may serve an array of communal projects.

But what happens when population genetic communities become part of political debates? If communal boundaries are products of methodological negotiation, how does the underlying ambiguity of communities and communal boundaries become mobilized in arguments for a politics of inclusion or exclusion as based on evolution? The following sections approach these questions through the idea of continental (European) and national (Finnish) genetic communities. I view both through the resonancies and discrepancies between the concept of population and the idea of community.

Continental Genes, Transcontinental Migrations

While commercial genetic ancestry tests seek to ground belonging on genetic relatedness and generate genetically framed forms of sociality, there is a clear gap between the idea of community and the idea of population. This is especially the case with mitochondrial and Y-chromosome tests. Sociality and communality take shape in the present, engendering ties among contemporary people who engage in the search of personalized ancestry. Population, in turn, is located primarily in the prehistoric past. Distinguished by their presumably unique combinations of ancestry informative markers, or their mitochondrial or Y-chromosome haplotypes, prehistoric populations are seen as the evolutionary origins from which the preconditions of modern communality arise. But what if population and community do coincide? This is the case with attempts to conceptuality modern Europeans as well as modern nation-states within Europe as distinct genetic populations. However, these two attempts are in tension. If population is seen as a continent-level phenomenon (e.g. Europeans as a genetically coherent population), then national communities do not appear easily as genetically meaningful populations. If population is seen as a nation-level phenomenon, then the modern inhabitants of a continent are unlikely to appear as a coherent genetic entity. These

tensions are a prime example of the role that temporality plays in producing difference: the further back we look in evolutionary time, the further we move from contemporary nations to questions of prehistoric migrations across continents.

In the years following the "discovery" of Mitochondrial Eve and Y-Chromosome Adam, the emergence and distribution of mitochondrial and Y-chromosome haplogroups across particular continents received growing attention. Researchers focused on the stretches of evolutionary history that led from the figure of Eve some 150,000–200,000 years ago in Africa to mitochondrial haplogroups specific to each continent (e.g. Cavalli-Sforza 1997). As we saw in the Roots for Real slide show above, these haplogroups are seen as connected not only through evolutionary time (the dynamics of gradual mutation known as molecular clock) but also through the spatial movement of prehistoric populations from Africa to Middle East, Asia, Australia, Oceania and Europe, and eventually to the Americas. Studies focusing on the genetic effects of such migrations provided the basis on which nationally framed genetic endeavors were gradually built. At the same time, technological development also complicated the relationship between continental and national genetic inheritance. With the introduction and routinization of high-throughput genome-wide analysis, populations are no longer conceptualized through patrilineal and matrilineal trajectories of movement. Instead, genome-wide approaches examining a wide range of ancestry informative markers and other molecular variation have rendered the relatedness of people and populations within both continents and nations considerably more complex than mitochondrial or Y-chromosome lineages alone would indicate (e.g. Bauchet et al. 2007; Novembre et al. 2008; Lao et al. 2008; Nelis et al. 2009; Balaresque et al. 2010). While these developments have without a doubt increased the accuracy of population genetic studies, they have also augmented the tensions between continental and national genetic frameworks.

The growing interest in continent-specific genetic characteristics since the late 1990s has given rise to attempts to imagine a fixed material connection between geographical location and genetic variation. A particularly vivid example of this trend is the popular science book *The Seven Daughters of Eve* by Bryan Sykes, the geneticist behind the genetic ancestry

company Oxford Ancestors. Published in 2001, the book explains and depicts the scientific search for mitochondrial haplogroups from which modern Europeans are descended. Sykes's text posits these seven haplogroups as "European" through several rhetorical means. First, the text suggests that each haplogroup has arisen around a "founder sequence" (Sykes 2001, 196). The language of "founder sequences" invokes ideas of founding members (in this case founding mothers) and the act of founding of a community, as if these new sequences had emerged as a result of a conscious decision to move to a new land and build a new society. It also implies that there would be a specific moment in prehistoric time when the foundation of the new genetic community was laid. This impression is further strengthened through references to "native Europeans" (Sykes 2001, 196). The phrase is problematic in two ways. It creates a division between native and nonnative modern Europeans, which posits white Europeans as "native" while rendering those who immigrated to Europe from other continents during the last several hundred years as nonnative. It also uses a politically invested term often reserved for indigenous populations such as Native Americans to describe European populations deeply involved in the discriminatory and exploitative practices of colonialism.

Second, Sykes's book appears to tie the seven mitochondrial haplogroups firmly to evolutionary time and geographical space by imagining the seven women who carried these mitochondrial signatures in their cells. Not only are these ancestral "mothers" given names: Ursula, Xenia, Helena, Velda, Tara, Katrine, and Jasmine—the same names that appear on the Oxford Ancestors website. They are also each given a full chapter in which Sykes the narrator imagines the circumstances of their lives and deaths. These are no dull descriptions of archeological finds or gene frequencies. Sykes produces emotionally charged narratives of, for example, how Ursula's two daughters, "[w]ith a last kiss, and with eyes full of tears," leave her to die in a cave as she cannot travel with the band any longer (Sykes 2001, 211), or how Xenia's parents save the weaker of her twin daughters from death by giving the baby to a young woman in a neighboring camp who had just lost her newborn son. These affectively invested fantasies connect the seven "European" haplogroups to specific proto-European locations while insisting that "almost everyone in Europe is

connected by an unbroken, almost umbilical thread" to these imagined, embodied women (Sykes 2001, 197). Furthermore, such fantasies mobilize DNA as a means of prosthetic memory explored in the previous chapter. Our mtDNA, revealed through genetic testing, emerges as able to carry us to the distant, previously unknowable past, as well as to bring the emotional circumstances of our newly discovered European ancestral mothers into the affective reach of the present moment. "Come with me now on a journey into the deep past," Sykes the narrator beckons us: "Guided by the unbroken genetic threads that link us to our ancestors, we can travel back to a time before the dawn of history, to a world of ice and snow, of bare mountains and endless plains, to meet these remarkable women—the Seven Daughters of Eve" (Sykes 2001, 201). The prosthetic nature of mtDNA is remarkable here. In addition to rendering the seven women unique, embodied, emotionally charged figures, it invokes an imagined yet tangible proto-European landscape that can be sensed through touch, smell, and sight.

While Sykes's way of connecting a presumably coherent European population living in the present to prehistoric populations migrating *within* Europe is rhetorically powerful and culturally resonant, the ease with which the two populations coincide is largely illusionary. The equation of the contemporary and prehistoric European populations is made possible through a series of exclusions. As suggested above, one is the definition of the modern European population in a way that excludes the extensive processes of migration into Europe that have taken place in the past millennium in particular. Only through this exclusion the idea of a direct connection between a modern European population and a prehistoric European one emerges as plausible. Another exclusion involves the stopping of evolutionary time within European borders. That is, although Sykes's book explores patterns of migration, his focus is within Europe. However, the patterns of migrations that lead to the emergence of the "European" haplogroups described by Sykes originate outside the borders of Europe in Africa, Middle East, and Asia. While, admittedly, Sykes's focus reflects the framing of the book as European ancestry, that very framing is an effect of the freezing of evolutionary time within particular temporal and spatial parameters. Just like modern Europeans presumably descend from the seven ancestral women, those women in turn descend from a line

of mothers who lived outside the borders of modern Europe. This draws attention to another key element: the invocation of "Europe" in the context of prehistory that precedes the concept of distinct, nameable continents. Finally, the connection between a modern and a prehistoric European population would look quite different had the book traced ancestry through other technologies such as Y-chromosome lineages or genome-wide approaches tracing an array of ancestry informative markers. While Sykes has indeed attempted writing Y-chromosome history in his 2003 book *Adam's Curse*, his patrilineal and matrilineal histories appear as parallel rather than epistemically challenging one another.[6]

Crucially, these same tensions underlie attempts to make a national population to cohere with an idea of a prehistoric population. That is, zooming in to more recent and more local evolutionary history does not resolve the problems inherent in the idea of the prehistorical foundations of a modern population present in Sykes's rendition of European prehistory. Like continents, nations have emerged as ways of conceptualizing difference and sameness quite recently and thus do not fit well within the dynamics of transcontinental and cross-regional migrations that organize human evolution. While nation-states that comprise an island and thus have clear physical boundaries—Iceland is a case in point—may appear as coherent entities, their histories, too, have been characterized by immigration, and their roots extend to other regions and other continents. Moreover, the idea of a national population as a coherent genetic population takes a different shape depending on the technologies, material, and statistical methods through which it is approached. The case of Finland and the genetic constitution of Finns will elucidate these issues.

Constructing Finnish Genetic Inheritance

Finland has a complicated relationship to Europe. Before gaining independence in 1917, Finland was first part of Sweden and, from 1809 until 1917, an autonomous Grand Duchy of the Russian Empire. Like many European countries in the nineteenth century, Finland developed its own form of national romanticism, which sought to establish the idea of a "Finnish people" and provide it with a distinct collective identity. The

construction of the Finnish people took place through the declaration of linguistic and cultural uniqueness, both important issues in distinguishing Finns from Swedes and Russians. However, with the rise of scientific theories of racial differences especially since the late eighteenth century, there was growing pressure to place Finns on the global map of racial hierarchies in a way that would help posit the geographically and economically marginalized country as a true nation. As nineteenth-century race theories often classified Finns as non-Europeans—for example, the famous German naturalist Johann Friedrich Blumenbach saw Finns as "Mongolian" rather than "Caucasian"—the project of making the Finnish people involved distancing Finns from the peoples of Siberia and East Asia, and aligning Finnishness with privileged white, primarily northwestern, Europeanness. This was an inherently precarious project in that *too much* Europeanness might undo the cherished idea of Finns as a distinct people that needed to form their own nation and govern themselves independently.

From these nineteenth-century negotiations of national identity and racial differences arose the view of Finns as inhabiting a unique position at the border of Europe and Asia. This assumption underlies twentieth-century scientific studies of population differences. Central to this representation is the idea of Finns as *isolated*, a view that downplayed the fact that Finland shares a land border with Russia, Norway, and Sweden, and that people with roots in Sweden or Russia have been part of Finnish society for centuries. In today's population genetic studies, this idea of isolation takes the shape of genetic exceptionality. For example, a 2008 study of genetic variation in Europe states that "the autosomal gene pool of extant human populations in Europe lacks sharp discontinuities with the exception of known isolates such as the Finns" (Lao et al. 2008, 1242). Articles ranging from 1990s Y-chromosome and mitochondrial studies (Kittles et al. 1998; Sajantila et al. 1996) to recent genome-wide analyses of thousands of ancestry informative markers (Nelis et al. 2009; Bauchet et al. 2007) repeat the idea of Finns as a genetically distinct population. This is highlighted through representational practices such as maplike illustrations of genetic distance between European populations (see, for example, Lao et al. 2008, 1243). At the same time, population geneticists highlight "[t]he high level of genetic homogeneity in Europe" (Nelis et al. 2009, 5)

and may refer to a European continental "population" in singular (Bauchet et al. 2007, 948). This framing reinforces the idea of a clear fit between prehistoric populations on the European continent and modern Europeans that organized Sykes's sentimental account of the seven ancestral mothers. It also posits the Finns, through their relative difference within the genetic sameness of the European population, as that which constitutes the very boundaries of Europeanness.

The idea of the Finnish population as genetically unique is further complicated by the phenomenon known as Finnish Disease Heritage (FDH). Introduced formally in the early 1970s, the concept reflected the observations by medical practitioners and researchers that some rare inherited diseases are unusually common in Finland compared to other countries, and there are even some new diseases that appear to be truly unique to Finland. In his extensive study of how the Finnish population came to be seen as a coherent entity useful for biomedical research, Aaro Tupasela (2016) identifies connections between the introduction of FDH and the nineteenth-century national romantic project. Tupasela coins the term *genetic romanticism* to capture the ways in which the FDH mobilized older national romantic narratives of Finnish roots in order to construct a genetically meaningful national population. Preexisting discourses of isolation gained new momentum in the process, as many rare diseases could be traced within individual, geographically localized families. Tupasela and Sakari Tamminen note that the concept of FDH played a key role in negotiating the genetic identity of Finns in Europe: "Despite FDH being a very heterogeneous group of disease, it has, in part, served to formulate a specific vision of Finns as homogenous yet European during the past fifty years" (Tupasela and Tamminen 2015, 412). Tupasela (2017) also shows how the FDH and the accompanying idea of a genetically homogenous population organize ongoing government-supported attempts to turn Finnish biobanks into a competitive resource for international biomedicine. What distinguishes Finnish biobanks from many other biobanks is the way they are framed as being able to bring together a unique national genetic inheritance, comprehensive health information available through the public healthcare system, extensive official records of family histories, and a public that is largely supportive of biomedical research. Indeed, it could be said that the "Finnish population" is a

product of social, cultural, and political forces as much as of the actual genetic characteristics carried in the cells of Finnish citizens.

While the FDH has generated powerful ways of branding and commercializing population-level biological information, the idea of genetically unique and homogenous nation relies on several exclusions and contradictions. First, as Tupasela (2017) points out, the construction of the Finnish population required leaving out recent immigrants, and often also tended to erase the indigenous populations of the nation, especially the Sami. Had the construction of the Finnish genetic population included indigenous groups and recent immigrants, the result would have likely been more diverse national genetic inheritance. This would have made visible the long history of people moving across regions and crossing what would be today borders between nations, a phenomenon that questions the assumption that nations are genetically meaningful entities. Second, and related to this, while the FDH seeks to trace the emergence of rare diseases through family histories, it appears to rely on a view of the Finnish population as frozen in time. As I argued in the case of Europe and the borders between continents, if we look further back in evolutionary time, boundaries between political and regional entities—regions, nations, continents—dissolve, as all populations (with the notable exception of Africans) have appeared in their current location through histories of migration. To put it slightly differently, the roots of the Finnish people are ultimately in other regions. Third, the positioning of inherited diseases as the source of genetic uniqueness invests the idea of national community with underlying uncertainty. Both national and evolutionary narratives tend to glorify reproductive success, that is, the continuation of reproductive trajectories from the past to the present to the future. Placing deleterious mutations in the heart of this dynamic as that which is reproduced undermines the striving for continuity and futurity in national and evolutionary narration. Although the construction of Finns as a genetically exceptional community follows the logic of evolutionary nostalgia by highlighting the role of roots as a source of true communality in the present, the past does not appear to guarantee futurity in the same way as it does, for example, in commercial genetic ancestry tests.[7]

Finally, despite the attempts to establish Finns as a homogenous population, there is a long tradition of seeing Finns as divided into several populations. This complicates the idea of Finnish genes as shared by all Finns and as unique to Finland (as opposed to having arrived from the neighboring countries). Genetic differences within Finland are registered in scientific studies that compare regions of Finland (see, for example, Nelis et al. 2009). Likewise, it was a central theme in the 2010 announcement by the Institute for Molecular Medicine Finland (FIMM) of the initial compilation of a genetic database called "Finnish Gene Atlas," and was highlighted in the ensuing media coverage (e.g. YLE 2010). The announcement of the "Finnish Gene Atlas" also gave rise to more extensive cultural explorations of differences within Finland, such as the article titled "West and East" in the monthly magazine of the leading Finnish newspaper *Helsingin Sanomat* (Malmberg 2010). The article frames the discovery of genetic differences in Finland within cultural narratives of how Eastern and Western Finns' attitudes toward food, work, and life in general differ. It also produces striking images demonstrating, for example, the difference between how Western and Eastern Finns cut (or refuse to cut) their lawns—the image of cut and uncut grass appears on the front cover of the magazine and is accompanied with the text: "two peoples." Interestingly, the narratives of Eastern and Western Finns that the article invokes portray Western Finns as connected to Swedes and Eastern Finns as connected to regions that are currently part of Russia. This portrayal highlights the importance of a history of migrations into the area that constitutes today the modern nation-state called Finland.

These contradictory tendencies toward establishing Finland as a genetically coherent entity, on the one hand, and identifying genetic differences within Finland and tracing them to neighboring regions, on the other, show how fragile the connection between a modern population and a prehistoric one is. Such connection is not a natural fact but a product of epistemic work. It needs to be maintained through acts of repetition involving the naturalization of particular scientific models and categories, such as the idea of the nation or its constitutive parts as genetically meaningful entities, as well as the mobilization of cultural narratives of the uniqueness of the modern population. Although the view of Finns as genetically exceptional and the view of Finns as genetically divided are

not necessarily mutually exclusive—Finns can be distinct from many European countries and yet display internal differences—they operate on different logics of connecting the present to the evolutionary past. That is, they organize genetic variation into different kinds of patterns of difference and sameness depending on what is seen as the unit of analysis—nation, regions within nation, a region spanning across a national border—and how boundaries between those units are conceptualized. This suggests that any claimed connection between a present population and a hypothesized past population always arises from a specific chain of technological interventions and discursive acts.

Ambiguous Communities

This ambiguity inherent in the relationship between imagined contemporary communities and prehistoric populations provides a rhetorical resource for various political projects of curtailing as well as extending belonging. Despite the ways in which national, regional, continental, and global patterns of genetic diversity seep into one another in population genetic technologies, population genetics can be brought to envision political projects of redefining community. In such acts of rewriting, ambiguity helps bring together a diverse and mutually contradictory set of cultural narratives of roots, destinies, and belonging in ways that produce an appearance of coherence. The debates and practices surrounding immigration in contemporary Europe provide a good example of this tendency. For example, the idea of evolution as a continuous process of migrations across continents and geographic regions throughout millennia can be turned quite effortlessly into a language of "native" Europeans, as we saw in Sykes's depiction of the seven European ancestral mothers. In fact, the idea of underlying migrations reinforces the sense of momentousness and foundationality associated with the mitochondrial European ancestors. Likewise, prehistoric migrations, despite their border-crossing nature, can be mobilized to support the idea that the majority population of a nation is in fact "indigenous" to the country, as Anne-Marie Fortier (2012) shows in her analysis of the "indigenization" of white Britons (discussed in Chap. 3 of this book). Importantly, Fortier notes that "[a]

lthough the explicit language of indigenousness in relation to some European populations may be confined to far right politics, the idea of a European indigenousness is not" (Fortier 2012, 154). Because population genetic narratives of human evolution are deeply entangled with discourses of prehistoric roots and moments of origins, patterns of migration that appear to challenge genetically grounded national communities can be invoked to enact precisely such a community. This rhetorical maneuver involves choosing which migrations count as real foundational events and which constitute insignificant genetic noise.

Two examples will help shed light on the range of political goals toward which the ambiguity of population genetic community can be mobilized: one draws on other researchers' work, the other one builds on my own observations. The first example highlights the entanglement of genetics and anti-immigration agendas. In the past 15 years, genetic models of community have become a normalized part of the managing of both European borders and national borders within Europe. The September 11, 2001, terrorist attacks provided a rationale for the institution of new tools of monitoring and controlling the movement of people across borders, including required sharing of data between national and EU-based databases (M'charek et al. 2014). In the past few years, the arrival of large numbers of refugees from Iraq, Afghanistan, and especially war-torn Syria to Europe has been followed by heated calls to further tighten the borders of the European Union as well as those of its member states. Many of the screening practices involved in border control build on the idea of genetic ties as a basis for citizenship and the right to cross borders. For example, genetic testing has become a normalized part of family reunification processes for those admitted to live in Europe or the United States and wishing to bring their families to live with them (Heinemann and Lemke 2012, 2014; Lee 2012). While such tests typically focus on genetic ties between parents and their offspring rather than population-level genetic similarities, they draw on the entanglement of kinship, gender, nation, and race, as Catherine Lee (2012) argues. According to Lee, while genetic tests used in family reunification cases are of intimate and deeply felt concern to individual people, they are also suggestive of the ways in which ideas of communities, roots, and belonging are being increasingly conceived through a geneticized logic of reproductive

relatedness. Such logic resonates with the idea of reproductive continuity that I located in the heart of prehistoric nostalgia in the previous chapter.

This entanglement of genetic kinship, nation, and race becomes visible in the Human Provenance Pilot Project (HPPP) in the United Kingdom in 2009–2010, which Richard Tutton, Christine Hauskeller, and Steve Sturdy (2014) have analyzed insightfully. The HPPP subjected people seeking asylum to genetic and isotope analyses in order to allegedly identify whether they actually came from the countries they claimed to be fleeing. The genetic analysis employed methods largely similar to the ones used in commercial genetic ancestry tests, but this time not to build a new community but to exclude from a national community. Tutton, Hauskeller, and Sturdy show that the tests would not be able establish the refugees' national origins and in fact were likely to lead to false conclusions: for instance, since haplotypes and ancestry informative markers are not unique to national populations, they cannot determine the "true" nationality of the immigrant. For my analysis, Tutton, Hauskeller, and Sturdy's study is particularly interesting because it demonstrates how the idea of population genetic community is gaining an institutionalized status as a basis of belonging. It also elucidates how the idea of population genetic community can be invoked in remarkably flexible ways to support not merely right-wing populism but also state-level anti-immigration policies. At the same time, the HPPP points to the slipperiness of the connection between community and population. While the justification for the tests draws on the assumption that modern nations (such as the refugee's country of origins) constitute coherent genetic entities, the technologies utilized are geared toward locating different types of origins: large prehistoric regions, often widely spread genetic clusters, or evolutionary migrations that cannot be captured on maps that insist on the epistemic primacy of borders between modern nation-states.

My second example illustrates how the idea of population genetic community is appropriated in antiracist and pro-immigration politics. While this case study comes from Finland, there are plenty of other examples from progressive-leaning discourse across Europe and North America. Like elsewhere in Europe, the arrival of Syrian and Iraqi refugees in Finland has been received with intensified and outspoken

expressions of xenophobia, including claims that the new migrants pose a threat to the genetic unity of the Finnish population. At the same time, those defending refugees' rights for asylum as human rights have often sought to turn the narrative of a homogenous Finnish population upside down with the help of population genetics. For example, the national broadcasting company YLE published a brief news article on how Finns involved in family genealogy are finding out through genetic ancestry tests that (in the interviewed genealogy enthusiast's words) "we are all immigrants" (Meriläinen 2016). Another news article on the YLE website describes how ethnically white Finnish high school students discovered through genetic ancestry tests that "Finnish inheritance is multicultural" and "international" (Holopainen 2017). A longer piece in the regional newspaper of Lapland, *Lapin Kansa*, provocatively titled "There is no Finnish people," evokes the idea of dramatic genetic differences between eastern and western parts of Finland to challenge the idea of a genetically unified nation (Tapio 2017). Common to all three articles is the emphasis that Finns share DNA beyond national borders, and that migration is not an exception but an organizing part of human existence.

An article titled "My Race" published on the website of the Finnish general interest magazine *Suomen Kuvalehti* fleshes out these tendencies (Penttilä 2016). The multimedia article combines a written account of three men's DNA analyses with video interviews, genetic maps, and information of the technical aspects of DNA analysis (such as differences between mitochondrial, Y-chromosome, and admixture analysis). The three men have all moved to Helsinki from elsewhere: one of them is a well-known novelist born in northern Finland, another one is a researcher born in the Kurdish region of Iran, and the third one is a radio host and politician born in Somalia. The politics of the article are made quite explicit through the portrayal of the three men as "Finns." The article also emphasizes that race is not a scientific category, that skin color does not reflect patterns of genetic difference, and that the human species shows much less genetic variation than many other species.

The *Suomen Kuvalehti* article posits antiracism as scientifically justified by evoking evolutionary temporality. Instead of insisting that white ethnic majorities are "indigenous" to the nation or "native" to the continent,

as we saw happen in the examples in the previous sections, the text highlights temporal trajectories reaching from modern individuals located within the nation-state known as Finland to prehistoric migrations from Africa across Middle East to Europe, and even further to the emergence of anatomically modern humans in the evolution of life. This temporal scope makes national and continental boundaries appear as mere administrative afterthoughts. At the same time, migration appears as a symbolic force: while the three men have all migrated to Helsinki, the genes they carry are products of a much more foundational diaspora arising from Mitochondrial Eve and Y-Chromosome Adam. Indeed, migration emerges as an ontological condition of humanity. Furthermore, these patterns of continuous migration are valuated through the explicit portrayal of the Middle East as the engine of culture and civilization. Such a portrayal challenges the populist racist portrayal of the Middle East and North Africa as less civilized and less evolved than Europe.

While communal boundaries and borders appear to collapse in the *Suomen Kuvalehti* article, this celebrated disintegration is ultimately precarious. Despite the article's emphasis on the evolutionary timescale and transcontinental migrations, the present moment is still viewed within the context of national community. Even though the article seeks to open and expand the idea of Finnishness by including members of racialized or ethnic minorities who were born outside Finland, the article reinforces the idea that genetics provides a foundational means of defining roots and belonging. It also suggests that genetic community is a meaningful way of conceptualizing the place of individuals within entities known as nations. While the emphasis on migrations may appear as liberating, the foregrounding of genetic ties carries unpredictable cultural baggage. As Catherine Lee's (2012) observations above suggest, the very idea of genetic kinship is inseparable from ideas of race, nation, reproduction, and sexuality. As I have argued throughout the previous chapters, evolutionary temporal trajectories and the geographic spread of specific molecular structures are organized on the assumption of successful reproduction, which excludes the ways of being and belonging that do not follow the logic of heterosexual reproduction. Depending on the chosen technologies, heterosexual reproduction is further narrowed down to the transmission of specific segments of genetic material through exclusively

maternal or paternal lineages, or to vague percentages of the geographic distribution of a person's overall genetic inheritance. Furthermore, the temporal investments of the *Suomen Kuvalehti* article could be easily rewritten as supporting anti-immigration arguments by locating foundational moments of migration not in Africa 100,000 years ago, or in Middle East 12,000 years ago, but in the settlement of first humans in the region known today as Finland. All in all, the article shows that while population genetics can provide rhetorical resources for constructing a genetic community in a nonracist way, such a construction is ultimately fragile.

The fundamental ambiguity of genetic community becomes perhaps most visible in the fact that both the border control measures analyzed by Tutton, Hauskeller, and Sturdy (2014) and the genetic tests used in the *Suomen Kuvalehti* article employ technologies familiar from commercial genetic ancestry tests. Indeed, the three men in the *Suomen Kuvalehti* article were tested by the American genetic ancestry company Family Tree DNA. Although genetic ancestry testing companies typically frame their products in terms of personal identity work and family genealogy, the clearly political uses of the same technologies in border control policies, on the one hand, and antiracist discourse, on the other, show that these technologies can be mobilized to serve a range of projects of imaging and enacting genetic communities.

Populations, Communities, and the Politics of Difference

I would like to conclude by addressing two questions that arise from the framing of this chapter. First, what is genetic community in the context of population genetics? And second, what is the relationship between population genetic community and politics? While the analysis of the cases discussed in the chapter have circled around these questions and highlighted some aspects central to them, a brief elaboration on population genetic community and its entanglement with politics will shed

further light on how population genetics is shaping belonging in contemporary societies.

The chapter has traced a range of biotechnological practices that mobilize population genetics to imagine and enact community. At the heart of these practices is an assumed connection between *community* and the population genetic concept *population*. My analysis has shown that the connection between the two concepts is highly ambivalent. Some practices, such as commercial genetic ancestry tests, posit community as a preexisting but previously invisible web of affective social relations in the present; at the same time, genetic ancestry tests are in fact what constitutes those communities in the first place. Population, by contrast, emerges as located in the prehistoric past in mitochondrial and Y-chromosome tests. The unfolding genetic communities in the present are seen as products of prehistoric populations, but there tends to remain a temporal and affective distinction between the two. Population genetic practices that seek to trace or guard the genetic roots of nations draw on a different relationship between population and community. National genetic projects in particular work from the premise that the modern nation constitutes a genetically meaningful entity. This premise aligns the modern population of the nation with prehistoric populations in the area, with the result that the temporal gap between modern and prehistoric populations seems to dissolve. This alignment of modern and prehistoric populations provides the basis for imaging national communities as tightly connected to localized prehistoric people. Furthermore, there are various constellations of population and community arising from the specific technologies used in the analysis. For example, as my analysis of commercial mitochondrial and Y-chromosome tests suggests, the tests' focus on matrilineal or patrilineal lineages genders the community that the tests allegedly discover.

The idea of genetic community is haunted by the multiple uses of the concept of population in population genetic research. In research projects, population can be defined on different geographical scales, ranging from specific regional populations (such as a localized cluster of a rare Y-chromosome haplotype) to transcontinental populations (such as the spread of mitochondrial haplogroups across North and South America). Likewise, temporal scope plays a crucial role in making populations:

population means quite different things in, say, studies of human diversity 5000 years ago and 50,000 years ago. Similarly, the material circumstances of population genetic knowledge production—tissue samples, cell lines, databases, reference sequences—play a key part in determining what counts as a population. This means that even when the connection between community and population seems straightforward, this appearance of naturalness emerges from technological practices and methodological choices. There is no "natural" fit between population and community. Instead, any connection between population and community needs to be maintained through continuous repetition. This applies to commercial genetic ancestry tests just as much as to Sykes's vision of European ancestry, the construction of FDH, the genetic determination of refugees' nationality, or antiracist celebration of the multicultural roots of nations.

Even when particular technological practices seem to establish a firm link between population and community, a slight shift of the analytical approach or discursive framing produces a new configuration of population and community. For example, distinctions between regions, nations, and continents are retrospective, that is, they emerge from the freezing of the evolutionary temporal scope to a specific moment in the past, or from the choice of methods or material. Viewed through a different temporal or methodological lens, distinctions between regions, nations, and continents would look different. The construction of Finns as genetically unique is a case in point. It demonstrates how the very idea of "Finnish genes" operates as a boundary-producing mechanism through which Europeanness on the one hand, and the presumably exceptional "Finnish population" on the other hand, are made. At the same time, the argument for two clearly distinct southwestern and northeastern Finnish subpopulations related, respectively, to Scandinavia and the eastern regions of Russia shows that a different way of conceptualizing boundaries produces other kinds of regional, national, and transnational genetic communities. Whereas the homogeneity of Finland arises through comparison to Europe, the internal heterogeneity of Finns is enacted through comparisons of northeastern and southwestern Finnish regions and their relation to neighboring genetic clusters beyond national borders.

If the role of *population* as a foundation of *community* is this unstable, how can believable and rhetorically appealing politics emerge around population genetic belonging? First of all, the various constellations of population and community draw on and reinforce a culturally celebrated understanding of genetic ties as epistemically privileged means of being and belonging. The different ways of enacting genetic community share the assumption that genetics can reveal fundamental truths about our existence and thus mold modern societies in foundational ways. This adds a sense of irrefutability and material concreteness to discourses of genetic community. Implicit in the technologies is the assumption, discussed in the previous chapter, that DNA is a historical witness to evolutionary roots otherwise invisible to us. This strengthens the idea that genetic ties constitute the ultimate connection between and across generations. Furthermore, this genetization of community and communal belonging is itself political in that it marginalizes culturally defined webs of belonging, such as political affiliations or friendships not based on shared genetic likeness. The affective temporal logic of evolutionary nostalgia further consolidates such politics of communal coherence and belonging. By turning to fantasized foundational moments of communal origins, evolutionary nostalgia seeks to reimagine the communal present and future as better, stronger, and more appealing than it might appear prior to the genetic analysis. While evolutionary nostalgia invests the idea of population genetic community with considerable affective appeal, releasing it from the perceived messiness of modern multicultural realities, the very need for evolutionary nostalgia to fortify genetic communities suggests that the coherence of genetic communities is fragile. At the same time, the organizing role of evolutionary nostalgia in both racist and antiracist discourse suggests that how narratives of genetic community manage the temporal connections between the past, present, and future is a political act. Slightly different ways of attaching genetic communities to evolutionary roots and destinies may result in glorification of insular and exclusionary identities, or in celebration of constantly unfolding, open-ended communal ties.

But politics does not need to be conscious in order to have significant consequences. The geneticization of communal belonging invokes an array of assumptions about race, nation, reproduction, and gender that

may not be intended by the speaker. Partly this results from the complex historical entanglements of race and nation with ideas of variation and population. As others have extensively shown (e.g. Reardon 2005), these histories cannot be undone by simply replacing race with variation or nation with population. At the same time, the implicit political underpinnings of the very idea of population genetic community are inseparable from the heteronormative reproductive logic of evolutionary continuity. As I argued in the previous chapter, queer critiques of the reproductive dynamic of evolutionary models are crucial because they make visible how the idea of forward-reaching temporality is structured on the assumption of successful reproductive acts. Furthermore, the specific technologies used in the construction of genetic communities also matter. While some approaches, such as admixture analysis, lead to a relatively stable view of genetic variation, other approaches, such as mitochondrial and Y-chromosome analyses, may produce a more dynamic view of evolving and shifting differences. However, movement, too, can be brought to support several mutually contradictory projects of enacting community. This becomes evident in the use of maps that tend to freeze convoluted and crisscrossing processes of migration into a set of arrows on the global map, or in how highlighting particular migrations over others engender different accounts of the past.

In an article on DNA analysis in family reunification applications, Torsten Heinemann and Thomas Lemke (2014) address the debate about biosociality and biological citizenship. They argue that while biosociality and biological citizenship have engendered new forms of transnational belonging and possibilities for activism, the geneticization of communities also curtails individuals' opportunities and disciplines their behavior. This is especially the case with those who inhabit marginalized social positions, such as refugees seeking to be united with their families in the new country. My analysis of population genetic communities has highlighted the *ambivalence* inherent in the idea of community and communality built on population genetic knowledge. I hope to have shown that the idea of population genetic community is neither inherently progressive nor inherently reactionary, nor does it always only limit nor always only enable creative revisions of belonging. Rather, the idea of genetic community can be mobilized to imagine and enact communal belonging on various levels, including personal, regional, national, continental, or

global forms of belonging. It can be made to support various political positions, ranging from racist and nationalist to antiracist and multicultural ones. This ultimate ambiguity of population genetic community is a key reason why population genetic narratives and imaginaries resonate so widely across the political and cultural spectrum in so many transnational locations.

Notes

1. This difference between mitochondrial and Y-chromosome tests means that only men can take the Y-chromosome test while anyone can have their mitochondria analyzed.
2. The link between Genghis Khan and a particular Y-chromosome haplotype is merely hypothetical, as neither Genghis Khan nor his known direct male descendants have left genetic material that could be tested. The Genghis Khan hypothesis is based on the observation that one Y-chromosome haplotype has gained considerable prominence within the area ruled once by Genghis Kahn.
3. While the ability to surprise is generally portrayed in a positive way on the websites, there are exceptions. Several sites warn customers that the tests might reveal, for example, that two siblings do not share the same father or mother. Also, companies like African Ancestry caution that 35% of African-American men seeking to establish their roots in Africa may find out that their Y chromosome belongs to a non-African haplogroup, especially a European one (African Ancestry 2017). This reflects the systematic sexual abuse of black women by white slave owners during slavery.
4. The authors write about the maplike visualization of their analysis of European genetic diversity: "The resulting figure bears a notable resemblance to a geographic map," and "indeed, a geographic map of Europe arises *naturally* as an efficient two-dimensional summary of genetic variation in Europeans" (Novembre et al. 2008, 98; emphasis mine). However, science studies scholars analyzing practices of knowledge production have shown that the naturalness of methods, models and representations is an effect of processes of routinization. See especially M'charek (2005).
5. In fact, processes of evolutionary change are complex and chaotic, and they can usually be traced only in retrospect. See, for example, Beer ([1983] 2000); O'Hara (1992); Oikkonen (2013).

6. For a discussion of *Adam's Curse*, see Oikkonen (2009).
7. For a more detailed discussion of how evolutionary narratives are haunted by the very possibility of "reproductive failure," see Chapter 4 of my book *Gender, Sexuality and Reproduction in Evolutionary Narratives* (Oikkonen 2013).

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6

Reflections on Methodology and Biotechnological Change

Discourses around population genetics are focused on the trope of discovering: discovering roots, discovering genetic markers that connect us to those roots, and discovering how we belong to the millennia of human evolution and the human diversity it has generated. Throughout this book, I have argued that genetic ancestry and evolutionary belonging are not discovered, they are made. They are made through sequencing technologies and computer programs; they are made through reference genomes and databases; they are made through the collection and circulation of biological material such as tissue or blood samples. But they are also made through cultural imaginaries, shifts in affective investments, variations of evolutionary narrative or narratives of biotechnological innovation, assumptions about intersectional differences such as gender, sexuality, race, or class, and a sense of temporal movement from the present to the prehistoric past and again to the future.

I have argued that these two sides of population genetic belonging are inseparable, and that they in fact mold one another. On the one hand, the specificity of scientific technologies and population genetic approaches shapes how belonging can be imagined and enacted. For example, focusing on mitochondrial and Y-chromosomal DNA tends to gender

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belonging in binary terms while investing evolution with a sense of linearity and temporal progression. On the other hand, these gendered evolutionary trajectories draw on, and are made possible by, the reproductive symbolism attached to linear time and the sense of nostalgic longing that often organizes the relationship between the past, present, and future in culture. In order to understand how population genetics is shaping belonging, we need to understand this conjoiner and entanglement of technological developments, material circumstances, epistemic premises, cultural narratives, circulating emotions, affective intensities, and assumptions about intersectional differences.

The book's methodological contribution has been to show in practice how combining a science studies approach to specific biotechnological practices and a cultural studies approach to underlying tendencies such as affective intensities or narrative commitments can enrich each other. Moreover, they can make visible tendencies in the studied phenomenon—belonging—that would otherwise likely escape the analysis. Through this interdisciplinary approach, I have shown how population genetic belonging is ambiguous and multiple. This ambiguity and multiplicity characterizes particular biotechnological formations: for example, the public and media debate about Cheddar Man mobilized personal, regional, and national narratives of belonging, while investing them with affectively charged discourses of masculinity and class. Ambiguity also underlies the ways in which a technology becomes framed and received over a period of time. For example, the figure of Mitochondrial Eve became embedded in a complex set of affective and narrative investments that moved from discourses of autonomous and racialized female sexuality to depictions of heteronormative and symbolically white courtship. These ambiguities and multiplicities of belonging were rendered visible by my focus on how technologies—in the above cases, mitochondrial analysis—and affective investments, cultural narratives, and imaginaries of gender, race, and kinship *coproduce* ancestry. This approach enabled me to locate tensions between the forms of belonging that have emerged around population genetics. For example, the narratives of regional, personal, and national belonging invoked in the media coverage of Cheddar Man were often in tension. Yet, these tensions, and the ambiguity of population genetic belonging that underlies them, have not reduced the

appeal of population genetics as a means of imagining and enacting belonging. In fact, this ultimate ambiguity appears to be precisely what makes population genetics such a powerful rhetorical resource across culture and society.

My analysis of population genetics and belonging has centered on temporality. Evolution is a temporal dynamic that produces difference, as evolution leads to the emergence of new species as well as variation between populations. For this reason, temporality is key to understanding how population genetics positions us in the universe and how it conceptualizes the ties between individuals and communities. This does not mean that space would be unimportant: as we saw in the migration maps produced by genetic ancestry testing companies, space is a necessary means through which temporality produces species-level and population-level differences. The temporal lens of my analysis has highlighted the intricate ways in which temporality organizes belonging. It makes visible how particular biotechnological approaches, such as mitochondrial, Y-chromosome, and genome-wide analyses, produce different temporal dynamics of belonging. While mitochondrial and Y-chromosome approaches engender temporal trajectories that connect the present to an imagined point of origins in the prehistoric past, genome-wide approaches often highlight present diversity rather than specific ties to evolutionary roots.

Furthermore, these technologies can be mobilized on different levels of temporal "resolution." Depending on whether the focus is on global, continental, national, or regional genetic variation, different kinds of temporal ties to the past arise. This became visible in how Finnish genetic inheritance has been conceptualized within a national framework, on the one hand, and within a continental and transnational framework, on the other. The analysis showed that Finns could be depicted as a genetically exceptional localized community, as two subpopulations with different histories, or as a group of individuals with unique ties to prehistoric global and continental migrations. Based on the choice of approach, such as mitochondrial, Y-chromosome, and genome-wide analyses, and the temporal framing of belonging, such as relatively recent regional or more distant transcontinental migrations, different patterns of variation and likeness emerge. This means that although evolutionary

trajectories appear to root communities in prehistory through the perceived precision of molecular detail, the multiplicity of analytical techniques and temporal resolution renders population genetic communities blurry. As a result, the idea of population genetic community can be invoked and incorporated in multiple affective economies and politics of difference.

The Making of Belonging Through Evolutionary Temporality

One of the most central aspects of population genetic belonging that my interdisciplinary approach has rendered visible is the temporal dynamic I call *evolutionary nostalgia*. I have argued that the very idea of population genetic belonging is organized on two-way longing that connects the affective present to the evolutionary past and again to an alternative, better present and a more fulfilling future. Evolutionary nostalgia challenges the common assumption that population genetic belonging is past-oriented. Instead, the texts and practices analyzed in the previous chapters indicate that the search for genetic roots is organized through a simultaneous longing to imagine and enact an affectively or politically more satisfactory present. Evolutionary nostalgia also operates as a promise of continuity and futurity. This promise arises from how evolutionary nostalgia manipulates time and mobilizes affect through a logic of heterosexual reproduction. That this reproductive logic is biological (involving the passing of genetic material to the next generation) as well as symbolic (involving a heterosexual union that stands for the whole community) became evident in the media coverage of Mitochondrial Eve and in the popular novel *People of the Raven*. Crucially, this reproductive logic at the heart of evolutionary nostalgia is exclusionary, as it leaves nonreproductive sexual arrangements, communal affiliations, and political alliances outside the affective imaginaries of belonging. Moreover, specific technologies, such as mitochondrial and Y-chromosome analyses, conceptualize reproduction (and thus evolutionary continuity) even more strictly by crafting temporal connections across generations through genetic material passed on only through matrilineal or patrilineal lineages.

This entanglement of temporality, nostalgia, futurity, reproduction, and technological practice could not have been untangled by focusing on technological practice or cultural discourses alone. The way in which technological practices (mitochondrial and Y-chromosome analyses) and cultural tendencies (future-oriented narrative longing) come together in the working of evolutionary nostalgia emphasizes the importance of an interdisciplinary approach that engages with both biotechnological practices and cultural phenomena. The same could be said about how DNA operates as a tool of making roots and belonging. As I have argued through the book, DNA is a curious object in that it is material and yet abstract: while it is the material manifestation of inheritance inside our cells, it is also a code for making bodies—and as such it could, at least theoretically, be revised. DNA is also shared and unique at the same time. Single nucleotide polymorphisms—specific molecular sites where people vary—are seldom unique to individuals; they are shared across populations. Yet DNA is seen as the very foundation of human individuality as even siblings differ considerably in their overall genetic makeup.

This ambivalence about DNA has made it a powerful cultural symbol. The idea of materiality and concreteness has aligned DNA with assumptions of precision, irrefutability, and unmediated access assigned to bioscientific research in culture. At the same time, the idea of abstraction and revisibility has made DNA all powerful: it appears as able to rewrite future through cloning, as well as to take us to the previously unknowable past through the concept of *molecular clock*. I have shown how these rhetorical tendencies come together in the idea of DNA as a historical witness to the foundational evolutionary events that modern humans and their archival records cannot remember. This posits population genetics as an epistemically privileged means of discovering who we really are and where we belong. Technological developments are also important. For example, the increasing feasibility of ancient DNA analysis in the past 10 years has strengthened the sense that the connection between us and prehistoric ancestors is indeed material rather than theoretical, and that DNA really is a prehistoric witness rather than a metaphor for scientific time travel. Again, it is only by bringing a cultural studies understanding of collective memory and temporality of genes in dialogue with a science studies analysis of population genetic practices

that the complexities of the trope of DNA as a historical witness are fleshed out.

The way in which evolutionary nostalgia mobilizes DNA as a historical witness renders population genetics an appealing rhetorical resource for a range of social and political projects. At the same time, this conjoiner of evolutionary temporality and the symbolic significance of DNA draws on another temporal arrangement that arises from actual scientific practice: DNA as an object that may unfold differently depending on the technologies and methods through which it is analyzed, as well as on the cultural and historical contexts in which it is brought. As the case of Michelle and Barack Obama's DNA demonstrated, this may engender ways of imaging alternative, multicultural realities and more harmonious societal futures. However, it may also reinforce nationalist and racist conceptualizations of communal roots and futures. The ongoing immigration debates in Europe and the different ways of viewing the "Finnish people" as nationally homogenous or inherently multicultural demonstrate that how DNA unfolds in different technological and research practices is not aligned with particular visions of genetically grounded communal belonging. Rather, population genetic technologies and methodological practices become connected to affective, narrative, discursive, and symbolic formations in multiple and often unpredictable ways. Yet these connections are not unlimited: technologies shape cultural narratives, while cultural narratives shape how technologies are made to trace ancestry. For instance, the case of Mitochondrial Eve shows how the introduction of mitochondrial analysis of human ancestry engendered ways of imagining gender, sexuality, and race as modes of evolutionary belonging. At the same time, these new imaginaries of gender, sexuality, and race influenced the eventual framing of Y-chromosome analysis as correcting the weaknesses of "Eve theory," and as providing Eve with a heterosexual partner and modern humans with a real, presumably deeply missed, founding father.

All in all, the conjoiner of evolutionary nostalgia, the ambiguous temporality of DNA, and the idea of unfolding genetic histories makes population genetics widely attractive across culture and society. This temporal dynamic invests the evolutionary past with a promise of an alternative present and a better future. It provides means of rooting communities in

the distant past, and establishes them as ancient and thus as presumably irrefutable. Perhaps most importantly, however, the temporal dynamic provides communities with a sense of continuity and future direction. This perceived future-oriented power of genetic ancestry, I believe, is a key aspect of the popularity of population genetic discourses and narratives of origins.

Tracing Biotechnological Change

The book has traced the history of nonmedical human population genetics from the late 1980s to the 2010s. The history that emerges from my analysis is not a coherent or comprehensive account of the field of population genetics and its social significance. I have engaged in cases and debates that I felt revealed unexpected, curious, or interesting aspects of how population genetics is shaping cultural imaginaries and vocabularies of belonging. However, when read together, many of the cases attest to larger patterns of biotechnological change around population genetic knowledge. I will briefly outline some of these patterns here. As my analysis of the case studies has focused on various constellations of temporality, affect, and intersectional differences, my discussion of biotechnological transformation reflects this focus.

The most obvious change that has taken place since the 1980s is the appearance of Y-chromosome analysis to complement the matrilineal focus of mitochondrial analysis in the 1990s, and the shift from mitochondrial and Y-chromosome analyses to genome-wide technologies during the first decade of the twenty-first century. The first of these changes organized the debate about Mitochondrial Eve and Y-Chromosome Adam. The second change underlies the reemergence of ancient DNA during the past decade as a celebrated tool of tracing evolutionary origins. But the pattern of transformation is not quite this smooth. While ancient DNA studies and research on genetic variation between modern populations have embraced genome-wide technologies, mitochondrial and Y-chromosome analyses still dominate the genetic ancestry testing business. A possible explanation for this is the perceived ability of mitochondrial and Y-chromosome analyses to engender direct material ties

between the test takers and their prehistoric roots. In other words, the language of mitochondrial and Y-chromosome ancestors resonates with the *personalized* focus of genetic ancestry testing and the goal of family genealogy to identify new ancestors. The gendering of mitochondrial and Y-chromosome lineages also fits with cultural ideas of family ties as gendered relationships. Thus, while developments in the study of ancient DNA may appear to suggest that technology drives transformation, genetic ancestry tests imply that other factors are at play as well. As genetic ancestry tests are widely used to various purposes, this means that mitochondrial and Y-chromosome testing persists also beyond personal genealogy projects: for example, the *Suomen Kuvalehti* article on the roots of the three modern Finns invoked mitochondrial and Y-chromosome haplogroups in the context of the debate about immigration and multiculturalism. The transformation of population genetic practices, then, is not straightforward: older images and discursive frameworks linger, insisting on the importance of older forms of technology.

My second and related observation is that affect structures technological and scientific transformation. This connection between affect and biotechnological change organized the heated scientific and cultural debate about Mitochondrial Eve, and was expanded on in Greg Egan's short story "Mitochondrial Eve," Hideaki Sena's horror novel *Parasite Eve*, and Margaret Drabble's novel *The Peppered Moth*. Affect and technological change are also entangled in the study of ancient DNA. The shift from mitochondrial lineages (the type of ancestry analyzed in Cheddar Man) to genome-wide sequencing (the technology eventually used in the analysis of the Kennewick remains) involved the downplaying of the idea of an affectively charged and foundationally gendered mitochondrial or Y-chromosome connection. Yet genome-wide sequencing of ancient DNA produced new kinds of embodied ancestries by detecting, for example, the eye color of the long-deceased ancestor whose body yielded the ancient DNA sample. This introduced a new constellation of affective investments that highlighted the capability of emerging technologies to produce evermore detailed and material accounts of the evolutionary past. Such an affective constellation is, of course, not completely new. Technologies have always generated awe and wonder, and have often been attributed almost magical qualities. Nevertheless, even when the

affective investments that surround genome-wide sequencing of ancient DNA draw on older entanglements of affect and technological development, they cannot be reduced to older patterns of biotechnological transformation: no technology was previously able to turn molecular detail into a potentially vivid image of a prehistoric pair of eyes.

The various constellations of affect and technological change are often entangled with intersectional differences. The debate about Mitochondrial Eve provides again an illustrative example, as technological development—mitochondrial analysis of human evolutionary origins and relatedness—became embedded in evolving affective investments centered on gender, sexuality, and race. Likewise, the media coverage of the Kennewick and Cheddar remains mobilized and reinforced complex constellations of cultural emotions and ethnic, racialized, classed, gendered, and regional differences. Furthermore, the affectively charged discourses surrounding Cheddar Man's facial reconstruction and his likeness to, or difference from, local pubgoers made visible how different constellations of affect and difference can coexist. Finally, affect and intersectionality organize population genetic technologies also on a structural level. As I have argued, genetic ancestry tests gender and racialize belonging through their focus on uniparental and geographically located ancestries. At the same time, they embed this gendered and racialized belonging within the affective dynamic of evolutionary nostalgia.

I am not suggesting that these constellations of affectively charged intersectional differences directly control biotechnological change. Yet biotechnological transformation cannot be separated from the affective organization of difference. This becomes visible in how specific population genetic practices operationalize particular sets of affect and difference. For example, the affective and intersectional investments of Y-chromosome lineages are radically different in commercial genetic ancestry tests and anti-immigration arguments for national purity. While commercial genetic ancestry tests are likely to embrace culturally approved forms of masculinity and ethnicity as a positive resource for harmonious belonging, anti-immigration discourses often invoke much darker undertones of hierarchical and aggressive gendered and racialized belonging. This highlights the importance of identifying variations in population genetic technologies' entanglements with affect and intersectional

difference. Such variations of affective and intersectional investments may help us understand why particular population genetic practices in society appear resistant or open to change.

The methodological approach developed in the book plays a key part in making visible the role of affect, temporality, and narrative in biotechnological change. While the methodology does not offer a systematic approach to biotechnological change, it provides a *dynamic* approach that is able to capture shifts, continuities, resonances, and tensions in complex and evolving technoscientific phenomena. Such an approach can trace connections between cultural representations of biotechnological change and underlying structural tendencies such as narrative commitments, temporal investments, or affective intensities. Crucially, it is precisely at this interface between cultural discourse and structural orientations that science generates new societal meanings and cultural resonances, which may render some processes of biotechnological change advisable and others undesirable. Furthermore, the methodological approach is able to move across cultural, technological, and transnational sites where technoscientific practices are produced, made sense of, or consumed. The approach is particularly sensitive to intangible and changing cultural phenomena, such as the circulation of affective investments across sites of technoscience, or the changing formations of intersectional difference across time. It provides a way of thinking how sites and practices are connected through their affective and narrative underpinnings, and how these underpinnings may shape how technologies travel across culture and society.

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